

Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
135						140					145						
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595	
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu		
150					155					160					165		
ggt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggg	gag	gca	gtt	gga	gca	tca	643	
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser		
				170					175					180			
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggg	gag	gtg	acc	gtg	gac	ctg	ggg	691	
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly		
			185					190					195				
gag	cac	acc	ctc	gtg	att	gcc	ggg	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739	
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
	215					220					225						
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc		
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
	295					300					305						
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt		
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg	gcc	gat	ggg	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggg	ttc		
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc		
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg		
1219																	

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu  
 360 365 370  
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc  
 1267  
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val  
 375 380 385  
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct  
 1315  
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala  
 390 395 400 405  
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc  
 1363  
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala  
 410 415 420  
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc  
 1411  
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile  
 425 430 435  
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac  
 1459  
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn  
 440 445 450  
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt  
 1507  
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly  
 455 460 465  
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc  
 1555  
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser  
 470 475 480 485  
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac  
 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
 490 495 500  
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
 1651  
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
 505 510 515  
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca  
 1699  
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala  
 520 525 530  
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt  
 1749  
 Gln Gln Gln Ala Leu Met Asp Thr Val His  
 535 540  
 gcg  
 1752

&lt;210&gt; 494

&lt;211&gt; 543

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 494

Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser  
 1 5 10 15

Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn  
 20 25 30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His  
 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala  
 50 55 60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala  
 65 70 75 80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile  
 85 90 95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr  
 100 105 110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala  
 115 120 125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu  
 130 135 140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala  
 145 150 155 160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu  
 165 170 175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val  
 180 185 190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala  
 195 200 205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr  
 210 215 220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu  
 225 230 235 240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro  
 245 250 255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu  
 260 265 270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr  
 275 280 285

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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290                               295                   300

Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305                               310                   315                   320

Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
                325                               330                   335

Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
                340                               345                   350

Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355                               360                   365

Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
 370                               375                   380

Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
 385                               390                   395                   400

Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
                405                               410                   415

Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
                420                               425                   430

Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
 435                               440                   445

Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
 450                               455                   460

Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
 465                               470                   475                   480

Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
                485                               490                   495

His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
                500                               505                   510

Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
 515                               520                   525

Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
 530                               535                   540

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&lt;210&gt; 495

&lt;211&gt; 1434

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1411)

&lt;223&gt; RXS02550

&lt;400&gt; 495

gatcttaggc agccgtggga ttacaccctt ttagagctag aacagtaaaa attcacccaa 60



tagctttcaa	ctacgcacac	aaagtggcaa	cattgagcgg	gtg	act	aca	gac	aag	115
				Val	Thr	Thr	Asp	Lys	
				1				5	
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg	163								
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala									
	10	15	20						
gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat	211								
Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp									
	25	30	35						
cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg	259								
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val									
	40	45	50						
gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag	307								
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys									
	55	60	65						
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg	355								
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val									
	70	75	80	85					
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc	403								
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser									
	90	95	100						
acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac	451								
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr									
	105	110	115						
gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta	499								
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Val Phe Leu									
	120	125	130						
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc	547								
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu									
	135	140	145						
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg	595								
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp									
	150	155	160	165					
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt	643								
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys									
	170	175	180						
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa	691								
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys									
	185	190	195						
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc	739								
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro									
	200	205	210						
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att	787								
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile									
	215	220	225						

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835  
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg  
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883  
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro  
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931  
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val  
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979  
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr  
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc  
 1027  
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu  
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga  
 1075  
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly  
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa  
 1123  
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu  
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc  
 1171  
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser  
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc  
 1219  
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro  
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc  
 1267  
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu  
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca  
 1315  
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
 1363  
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag  
 1411  
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
 425 430 435

tagtagttgt taggattcac cac  
1434

<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn  
1 5 10 15

Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr  
20 25 30

Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu  
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly  
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe  
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr  
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala  
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val  
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr  
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro  
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro  
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu  
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile  
195 200 205

Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu  
210 215 220

Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp  
225 230 235 240

Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu  
245 250 255

Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser  
260 265 270

[illegible]

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<210> 497
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1057)
<223> RXS02319
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<400> 497
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agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115
Met Ser Asn Tyr Ser
1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

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40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct  
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
310 315

aaa  
1080

<210> 498

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 498

Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala  
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Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His  
20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg  
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210	215	220	
Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp			
225	230	235	240
His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn			
	245	250	255
Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu			
	260	265	270
Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr			
	275	280	285
Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe			
	290	295	300
Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr			
305	310	315	
<210> 499			
<211> 384			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
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<222> (101)..(361)			
<223> RXS02908			
<400> 499			
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		Leu Lys Leu His Pro	5
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163			
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala	10	15	20
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211			
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala	25	30	35
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259			
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp	40	45	50
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307			
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser	55	60	65
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355			
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys	70	75	80
ctg ttt tagtcttcat tcttgctggc tgc 384			
Leu Phe			

<210> 500  
 <211> 87  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 500  
 Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys  
     1                    5                    10                    15  
 Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly  
                     20                    25                    30  
 Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val  
                     35                    40                    45  
 Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu  
     50                    55                    60  
 Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg  
     65                    70                    75                    80  
 Arg Ala Ile Ala Lys Leu Phe  
                     85

<210> 501  
 <211> 775  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(775)  
 <223> RXS03003

<400> 501  
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 caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115  
   Met Thr Ser Arg Thr  
   1                    5  
 ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tgc ctc gct tcc 163  
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser  
                     10                    15                    20  
 gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211  
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser  
                     25                    30                    35  
 gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259  
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu  
                     40                    45                    50  
 gca gaa gca gcg ggg ttt tgc ggt tac cct caa acc atc ggc acc ccg 307  
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro  
     55                    60                    65  
 gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355



Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met  
 70 75 80 85  
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403  
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu  
 90 95 100  
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451  
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val  
 105 110 115  
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499  
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala  
 120 125 130  
 gga tgc acc gtg ttg cgt tct gat tgc ctg ttt aag ctc ggc ccg cag 547  
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
 135 140 145  
 atc ccg tgc atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595  
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
 150 155 160 165  
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
 170 175 180  
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
 185 190 195  
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739  
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp  
 200 205 210  
 ggc gac cac acc aac ttg atc gcc att cac tgc ctg 775  
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu  
 215 220 225  
 <210> 502  
 <211> 225  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 502  
 Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp  
 1 5 10 15  
 Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly  
 20 25 30  
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser  
 35 40 45  
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
 50 55 60  
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80

Arg	Arg	Tyr	Asn	Met	Thr	Lys	Leu	Val	Asp	Ala	Ser	Leu	Leu	Pro	Val		
				85					90					95			
Val	Gly	Thr	Lys	Glu	Ala	Ile	Ala	Leu	Leu	Pro	Phe	Ala	Leu	Gly	Ile		
				100					105					110			
Ser	Gly	Thr	Val	Val	Ile	Pro	Glu	Ile	Ala	Tyr	Pro	Thr	Tyr	Glu	Val		
				115					120					125			
Ala	Val	Val	Ala	Ala	Gly	Cys	Thr	Val	Leu	Arg	Ser	Asp	Ser	Leu	Phe		
				130					135					140			
Lys	Leu	Gly	Pro	Gln	Ile	Pro	Ser	Met	Met	Phe	Ile	Asn	Ser	Pro	Ser		
145					150					155					160		
Asn	Pro	Thr	Gly	Lys	Val	Leu	Gly	Ile	Pro	His	Leu	Arg	Lys	Val	Val		
				165					170					175			
Lys	Trp	Ala	Gln	Glu	Asn	Asn	Val	Ile	Leu	Ala	Ala	Asp	Glu	Cys	Tyr		
				180					185					190			
Leu	Gly	Leu	Gly	Trp	Asp	Asp	Glu	Asn	Pro	Pro	Ile	Ser	Ile	Leu	Asp		
				195					200					205			
Pro	Arg	Val	Cys	Asp	Gly	Asp	His	Thr	Asn	Leu	Ile	Ala	Ile	His	Ser		
				210					215					220			
Leu																	
225																	

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<210> 503
<211> 390
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101) .. (367)  
<223> RXS03026
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cgaactagcc ccccaacaac aattagaaat ggaacctaaa atg cct gga aaa att 115  
Met Pro Gly Lys Ile  
1 5

ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163  
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro  
10 15 20

gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211  
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr  
25 30 35

gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259  
Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn  
40 45 50

cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307

His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
 55 60 65  
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355  
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg  
 70 75 80 85  
 ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390  
 Phe Trp Met Leu

<210> 504  
 <211> 89  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 504  
 Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu  
 1 5 10 15  
 Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val  
 20 25 30  
 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu  
 35 40 45  
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn  
 50 55 60  
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr  
 65 70 75 80  
 Thr Leu Arg Trp Arg Phe Trp Met Leu  
 85

<210> 505  
 <211> 621  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(598)  
 <223> RXS03074

<400> 505  
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 tagcaggaca agcataactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
 Met Thr Gln Ser Ala  
 1 5  
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
 40 45 50  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
 55 60 65  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
 70 75 80 85  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
 90 95 100  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
 105 110 115  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
 120 125 130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
 135 140 145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
 150 155 160 165  
 cag taatttggtt tgacgacgca gta 621  
 Gln

&lt;210&gt; 506

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 506

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
 1 5 10 15  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
 20 25 30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
 35 40 45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
 50 55 60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
 65 70 75 80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
 85 90 95

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Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
      100                      105                      110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
      115                      120                      125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
      130                      135                      140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
      145                      150                      155                      160

Glu Ala Pro Ile Lys Gln
      165

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<210> 507
<211> 3075
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(3052)
<223> RXC01434

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aacactgcca acacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg 115
              Val Leu Gly Ala Val
              1                      5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
              10                      15                      20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
              25                      30                      35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
              40                      45                      50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307
Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
              55                      60                      65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355
Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
              70                      75                      80                      85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
              90                      95                      100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451
Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
              105                      110                      115

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ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
120 125 130	
gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc	547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt	883
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
250 255 260	
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg	931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac	979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
280 285 290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	
1027	
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	
295 300 305	
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg	
1075	
Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	
310 315 320 325	
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc	
1123	
Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile	
330 335 340	

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg  
 1171  
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu  
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac  
 1219  
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn  
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc  
 1267  
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg  
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg  
 1315  
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu  
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg  
 1363  
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu  
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta  
 1411  
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu  
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc  
 1459  
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe  
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc  
 1507  
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt  
 1555  
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
 1747  
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc  
 1795  
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala  
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc  
 1843  
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala  
 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag  
 1891  
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta  
 1939  
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg  
 1987  
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val  
 615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt  
 2035  
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly  
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc  
 2083  
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr  
 650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag  
 2131  
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys  
 665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg  
 2179  
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc  
 2227  
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala  
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc  
 2275  
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
 710 715 720 725



aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc  
 2323  
 Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro  
                     730                    735                    740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc  
 2371  
 Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr  
                     745                    750                    755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct  
 2419  
 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro  
                     760                    765                    770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg  
 2467  
 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met  
                     775                    780                    785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc  
 2515  
 Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala  
                     790                    795                    800                    805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa  
 2563  
 Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln  
                     810                    815                    820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct  
 2611  
 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
                     825                    830                    835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat  
 2659  
 Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
                     840                    845                    850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc  
 2707  
 Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
                     855                    860                    865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc  
 2755  
 Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser  
                     870                    875                    880                    885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc  
 2803  
 Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser  
                     890                    895                    900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc  
 2851  
 Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala  
                     905                    910                    915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat  
 2899  
 Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
           920                  925                  930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg  
 2947  
 Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
           935                  940                  945

ggc cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca  
 2995  
 Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
           950                  955                  960                  965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt  
 3043  
 Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
                   970                  975                  980

gtt ggt tgg taaattacgc gtttgtgatt gac  
 3075  
 Val Gly Trp

<210> 508  
 <211> 984  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 508  
 Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg  
   1                  5                  10                  15  
 Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu  
                   20                  25                  30  
 Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
           35                  40                  45  
 Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln  
           50                  55                  60  
 Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln  
           65                  70                  75                  80  
 Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
                   85                  90                  95  
 Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
           100                  105                  110  
 Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu  
           115                  120                  125  
 His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
           130                  135                  140  
 Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
           145                  150                  155                  160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
 165 170 175  
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
 180 185 190  
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
 195 200 205  
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met  
 210 215 220  
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala  
 225 230 235 240  
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala  
 245 250 255  
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
 260 265 270  
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn  
 275 280 285  
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu  
 290 295 300  
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu  
 305 310 315 320  
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr  
 325 330 335  
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser  
 340 345 350  
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
 435 440 445  
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
 485 490 495  
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
 500 505 510  
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
 515 520 525  
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
 530 535 540  
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
 610 615 620  
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
 660 665 670  
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
 675 680 685  
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu  
 705 710 715 720  
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala  
 725 730 735  
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
 740 745 750  
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu  
 755 760 765  
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
 770 775 780  
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val  
 785 790 795 800  
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

805										810					815				
Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser				
			820					825					830						
Ala	Thr	Pro	Glu	Pro	Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln				
		835					840					845							
Ala	Arg	Thr	Trp	Asp	Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr				
	850					855					860								
Asp	Gly	Asn	Thr	Ser	Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu				
865					870				875						880				
Leu	Val	Asp	Leu	Ser	Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr				
				885					890					895					
Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr				
			900					905					910						
Ala	Phe	Asn	Asp	Ala	Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile				
		915					920					925							
Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp				
	930					935					940								
Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp				
945					950				955						960				
Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile				
				965					970					975					
Ala	Glu	Val	Gln	Leu	Val	Gly	Trp												
				980															

&lt;210&gt; 509

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; RXC02080

&lt;400&gt; 509

cgtaaattcg aagcgagctt ctaattctag caagcttggt gatggagtat cctgcaaaaa 60

tttgtcctgt	tgcttattgt	gcaggaattc	ggaggcggac	atg	tca	atc	gag	tgg	115
				Met	Ser	Ile	Glu	Trp	
				1				5	

tta	caa	att	gtt	gaa	tta	gga	gcg	atc	ttt	ggt	gca	ggt	ttc	ctc	gca	163
Leu	Gln	Ile	Val	Glu	Leu	Gly	Ala	Ile	Phe	Gly	Ala	Gly	Phe	Leu	Ala	
			10					15						20		

gga	agc	atc	aat	gta	att	gtc	gga	gca	gga	aca	tta	gtg	tcg	ttt	cct	211
Gly	Ser	Ile	Asn	Val	Ile	Val	Gly	Ala	Gly	Thr	Leu	Val	Ser	Phe	Pro	
			25				30						35			

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
120 125 130	
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg	787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
250 255 260	
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc	930
Thr Val Ile Val Met Thr Ile Gly	
265	

&lt;210&gt; 510

&lt;211&gt; 269

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 510

Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly  
 1 5 10 15

Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr  
 20 25 30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr  
 35 40 45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly  
 50 55 60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg  
 65 70 75 80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu  
 85 90 95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu  
 100 105 110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys  
 115 120 125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln  
 130 135 140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala  
 145 150 155 160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile  
 165 170 175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu  
 180 185 190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala  
 195 200 205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr  
 210 215 220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly  
 225 230 235 240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val  
 245 250 255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly  
 260 265

&lt;210&gt; 511

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(646)

&lt;223&gt; RXC02789

&lt;400&gt; 511

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ttcttccgta cggtatgct taaaagctaa atttgtcttt gtgccttgca acacattaat 60

ttcttaacac taaacaatgg aaaggtaagc ggggtttttct atg aag gtt tcc gcc 115
                                         Met Lys Val Ser Ala
                                         1      5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                        10                        15                        20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                        25                        30                        35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
                        40                        45                        50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                        55                        60                        65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                        70                        75                        80                        85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                        90                        95                        100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                        105                        110                        115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                        120                        125                        130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                        135                        140                        145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                        150                        155                        160                        165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                        170                        175                        180

gga tgaaccaaat ccgaaaccgc cgg 669
Gly

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<210> 512
<211> 182
<212> PRT
<213> Corynebacterium glutamicum
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[illegible]

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<210> 513
<211> 903
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(880)  
<223> RXC02295
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<400> 513
ttcccatgct aatccgcgaa atgggcactt caacagccat atactttaaa caacacaaat 60

gatgcaagac tgataaccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta    115
                                     Met Gly Leu Glu Leu
                                      1             5
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gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	163
10 15 20	
tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg Trp Ile Asp Ala Val Ile Gly Gly Gly Leu Val Leu Ile Pro Leu	211
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	259
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Phe Thr Leu	307
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	355
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	403
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	451
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	499
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	547
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	595
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	643
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	691
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	739
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	787
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	835
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880  
 Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met  
                   250                  255                  260

tagataagtc ggggcaaact cta 903

<210> 514

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 514

Met Gly Leu Glu Leu Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly  
   1                  5                  10                  15

Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu  
                   20                  25                  30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val  
                   35                  40                  45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
                   50                  55                  60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
   65                  70                  75                  80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
                   85                  90                  95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
                   100                  105                  110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
                   115                  120                  125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
                   130                  135                  140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
   145                  150                  155                  160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
                   165                  170                  175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
                   180                  185                  190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
                   195                  200                  205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
                   210                  215                  220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
   225                  230                  235                  240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln  
                   245                  250                  255

Ile Gln Gly Met  
260

<210> 515  
<211> 1132  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1132)  
<223> RXN03063

<400> 515  
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acctagacaa cagtttgtat ctcacctcac aggaggaacc gtg gaa gat ctc tca 115  
Val Glu Asp Leu Ser  
1 5  
tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163  
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro  
10 15 20  
aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211  
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala  
25 30 35  
ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259  
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile  
40 45 50  
ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307  
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile  
55 60 65  
gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355  
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val  
70 75 80 85  
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403  
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro  
90 95 100  
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451  
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro  
105 110 115  
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499  
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala  
120 125 130  
gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547  
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala  
135 140 145  
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595  
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met  
150 155 160 165

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gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643
Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu
170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691
Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly
185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739
Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser
200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787
Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln
215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835
Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile
230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883
Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile
250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931
Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu
265 270 275

ggg gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979
Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly
280 285 290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc
1027
Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro
295 300 305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc
1075
Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys
310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag
1123
Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu Gln Ala Asp Leu Lys
330 335 340

acc cgc gcg
1132
Thr Arg Ala

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&lt;210&gt; 516

&lt;211&gt; 344

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 516

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Val Glu Asp Leu Ser Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu
1 5 10 15

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Gln Val Pro Gly Pro Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala  
                   20                                  25                                  30  
 Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp  
                   35                                  40                                  45  
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp  
                   50                                  55                                  60  
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala  
                   65                                  70                                  75                                  80  
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys  
                                   85                                  90                                  95  
 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu  
                                   100                                  105                                  110  
 Asn Ala Leu Thr Pro Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn  
                   115                                  120                                  125  
 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr  
                   130                                  135                                  140  
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg  
                   145                                  150                                  155                                  160  
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser  
                                   165                                  170                                  175  
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr  
                                   180                                  185                                  190  
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile  
                   195                                  200                                  205  
 Ser Val Ile Glu Ser Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val  
                   210                                  215                                  220  
 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly  
                   225                                  230                                  235                                  240  
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe  
                                   245                                  250                                  255  
 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe  
                                   260                                  265                                  270  
 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys  
                   275                                  280                                  285  
 Gly Ile Ala Gly Gly Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu  
                   290                                  295                                  300  
 Ile Met Asp Ala Pro Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly  
                   305                                  310                                  315                                  320  
 Asn Pro Val Ala Cys Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu  
                                   325                                  330                                  335

Gln Ala Asp Leu Lys Thr Arg Ala  
340

<210> 517  
<211> 1491  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1468)  
<223> RXN02970

<400> 517  
aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60  
ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115  
Leu Ala Leu Lys Gly  
1 5  
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
10 15 20  
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
25 30 35  
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
40 45 50  
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
55 60 65  
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
70 75 80 85  
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
90 95 100  
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
105 110 115  
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
120 125 130  
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
135 140 145  
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	



gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
1363

Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg  
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
440 445 450

gcg ttg ttc taagttttct agataacaag gcc  
1491

Ala Leu Phe  
455

<210> 518

<211> 456

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 518

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

145		150		155		160
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg						
		165		170		175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro						
		180		185		190
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys						
		195		200		205
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala						
		210		215		220
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly						
		225		230		235
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys						
		245		250		255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe						
		260		265		270
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe						
		275		280		285
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala						
		290		295		300
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly						
		305		310		315
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala						
		325		330		335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile						
		340		345		350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu						
		355		360		365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile						
		370		375		380
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala						
		385		390		395
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser						
		405		410		415
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu						
		420		425		430
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu						
		435		440		445
Leu Thr Phe Ala Gly Ala Leu Phe						
		450		455		

&lt;210&gt; 519

&lt;211&gt; 1330

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1330)

&lt;223&gt; FRXA01009

&lt;400&gt; 519

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aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgagggtgag 60

ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
                                   Leu Ala Leu Lys Gly
                                   1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                                   10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                                   25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                                   40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                                   55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                                   70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                                   90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                                   105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                                   120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                                   135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                                   150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                                   170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

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Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
			185					190					195				
tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
		200					205					210					
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
		215				220					225						
atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230					235					240				245			
gca	ggg	tac	tta	aat	ggc	gtg	cgc	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250					255					260			
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270					275				
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
		280					285					290					
acc	ttc	gcc	aag	ggg	gtt	aac	gca	ggg	tac	gcc	cca	ctc	ggg	ggc	atc		
1027																	
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile		
		295				300					305						
gtg	atg	acc	caa	tca	atc	cgc	gat	acc	ttc	gga	tca	gag	gca	tac	tcc		
1075																	
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
310					315					320					325		
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gcc	aag		
1123																	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
				330					335					340			
gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct		
1171																	
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala		
			345					350					355				
cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa		
1219																	
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu		
		360					365					370					
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca		
1267																	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
		375				380					385						
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggg	gct	gca	gaa		
1315																	
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu		
390					395					400					405		

ttc aag gaa cgc ggc  
 1330  
 Phe Lys Glu Arg Gly  
 410

<210> 520  
 <211> 410  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 520  
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 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
 20 25 30  
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
                   260                                  265                                  270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
                   275                                  280                                  285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
                   290                                  295                                  300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
                   305                                  310                                  315                                  320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
                                   325                                  330                                  335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
                                   340                                  345                                  350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
                   355                                  360                                  365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
                   370                                  375                                  380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
                   385                                  390                                  395                                  400  
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly  
                                   405                                  410

&lt;210&gt; 521

&lt;211&gt; 1998

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1975)

&lt;223&gt; RXA01551

&lt;400&gt; 521

cactacgtag gcgtaccca ccatcaccgc gtcgaaaagc gccctctctt aacccccgca 60

agggggtaac ttttacgcgc acgcgtgcaa cgcgctagtt ttg aag gca gtc ccc 115  
   Leu Lys Ala Val Pro  
   1                                  5

acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163  
 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala  
                                   10                                  15                                  20

ccg ttt gaa cct gtc cgg tta gca ccg gcg aag gaa gag agg aat ggt 211  
 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly  
                   25                                  30                                  35

gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259  
 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser  
                   40                                  45                                  50

ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307

Pro	Ile	Arg	Lys	Asp	Gly	Leu	Glu	Val	Pro	Glu	Thr	Glu	Ile	Arg	Leu	
	55					60					65					
gat	gac	tcg	cca	agc	ggc	ccc	aac	gaa	ccc	ttc	cgc	atc	tac	cgc	acc	355
Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	Arg	Ile	Tyr	Arg	Thr	
	70				75				80						85	
cgt	ggc	cca	gaa	acc	aac	ccc	aag	cag	gga	ctt	ccg	cgg	ctg	cgc	gag	403
Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	Pro	Arg	Leu	Arg	Glu	
				90					95					100		
tca	tgg	atc	acc	gcc	cgc	ggc	gac	gtt	gcc	acc	tat	cag	ggg	cgc	gag	451
Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	Tyr	Gln	Gly	Arg	Glu	
			105					110					115			
cgt	ttg	ctt	atc	gac	gac	ggc	cgc	tcg	gca	atg	cgt	cga	ggg	caa	gct	499
Arg	Leu	Leu	Ile	Asp	Asp	Gly	Arg	Ser	Ala	Met	Arg	Arg	Gly	Gln	Ala	
	120					125						130				
tcg	gct	gag	tgg	aaa	ggc	caa	aaa	cca	gct	cct	ttg	aag	gcg	cta	cct	547
Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	Leu	Lys	Ala	Leu	Pro	
	135					140					145					
ggc	aaa	aga	gtc	acc	caa	atg	gcc	tat	gca	cgt	gct	ggc	gtg	att	act	595
Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr	
	150				155				160						165	
cgt	gaa	atg	gag	ttt	gta	gcg	ctg	cgc	gaa	cac	gtt	gat	gcg	gag	ttt	643
Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe	
				170					175					180		
gtg	cgc	tct	gag	gtg	gcg	cgc	ggg	cgg	gcc	att	att	ccc	aac	aac	gtc	691
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val	
			185				190						195			
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggg	cgc	aaa	ttt	ttg	acc	739
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr	
		200					205					210				
aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787
Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu	
	215					220					225					
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggg	gcc	gat	acc	835
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr	
	230				235					240				245		
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883
Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp	
				250					255					260		
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931
Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln	
			265				270						275			
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val	
	280					285						290				
ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg	
																1027

Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met  
 295 300 305  
 acc atc cac gcc ggc gtc ctg ctg gct tat atc cca ctg act acc cgt  
 1075  
 Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg  
 310 315 320 325  
 cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg  
 1123  
 Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp  
 330 335 340  
 tgt ctg gcg cat cac cgc gaa tca ttc ctc tac gag cat ttc gac gag  
 1171  
 Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu  
 345 350 355  
 ctg tgc gaa atc ttt gca caa tat gac gtc gca ttc tcc ctc ggt gat  
 1219  
 Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp  
 360 365 370  
 ggc cta cgc ccc gga tcg ctt gcc gat gcc aac gac gcc gcg caa ttc  
 1267  
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe  
 375 380 385  
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac  
 1315  
 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr  
 390 395 400 405  
 gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg  
 1363  
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met  
 410 415 420  
 atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct  
 1411  
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro  
 425 430 435  
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac  
 1459  
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp  
 440 445 450  
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc  
 1507  
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr  
 455 460 465  
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac  
 1555  
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn  
 470 475 480 485  
 cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac  
 1603  
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His



490 495 500  
 gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac  
 1651  
 Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp  
 505 510 515  
 gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg  
 1699  
 Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala  
 520 525 530  
 ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg  
 1747  
 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu  
 535 540 545  
 ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg  
 1795  
 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro  
 550 555 560 565  
 aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc  
 1843  
 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly  
 570 575 580  
 gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt  
 1891  
 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser  
 585 590 595  
 gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg  
 1939  
 Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg  
 600 605 610  
 gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc  
 1985  
 Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg Arg  
 615 620 625  
 gatcccagat agc  
 1998

&lt;210&gt; 522

&lt;211&gt; 625

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 522

Leu Lys Ala Val Pro Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu  
 1 5 10 15  
 Ile Ala Ala Arg Ala Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys  
 20 25 30  
 Glu Glu Arg Asn Gly Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro  
 35 40 45

Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu  
 50 55 60  
 Thr Glu Ile Arg Leu Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe  
 65 70 75 80  
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu  
 85 90 95  
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr  
 100 105 110  
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met  
 115 120 125  
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro  
 130 135 140  
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg  
 145 150 155 160  
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His  
 165 170 175  
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile  
 180 185 190  
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly  
 195 200 205  
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val  
 210 215 220  
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg  
 225 230 235 240  
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His  
 245 250 255  
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr  
 260 265 270  
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp  
 275 280 285  
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln  
 290 295 300  
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile  
 305 310 315 320  
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser  
 325 330 335  
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr  
 340 345 350  
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala  
 355 360 365  
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370                      375                      380  
 Asp Ala Ala Gln Phe Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln  
 385                      390                      395                      400  
 Arg Ala Trp Glu Tyr Asp Val Gln Val Met Val Glu Gly Pro Gly His  
                     405                      410                      415  
 Val Pro Leu Asn Met Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp  
                     420                      425                      430  
 Ala Ala Asp Ala Pro Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile  
                     435                      440                      445  
 Ala Pro Gly Tyr Asp His Ile Thr Ser Ala Ile Gly Ala Ala His Ile  
                     450                      455                      460  
 Ala Met Gly Gly Thr Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His  
 465                      470                      475                      480  
 Leu Gly Leu Pro Asn Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr  
                     485                      490                      495  
 Lys Leu Ala Ala His Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala  
                     500                      505                      510  
 Arg Ala Trp Asp Asp Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp  
                     515                      520                      525  
 Asn Asp Gln Phe Ala Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr  
 530                      535                      540  
 His Asp Glu Thr Leu Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys  
 545                      550                      555                      560  
 Ser Met Cys Gly Pro Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile  
                     565                      570                      575  
 Arg Asp Met Phe Gly Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val  
                     580                      585                      590  
 Gly Asp Ser Ser Ser Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met  
                     595                      600                      605  
 Ala Glu Lys Ser Arg Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg  
                     610                      615                      620  
 Arg  
 625

<210> 523  
 <211> 1013  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(990)  
 <223> RXA01019

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<400> 523
act ttg gcg cac tca ctt tca ttc ccg gat tcg ctt cgc gac ggg cca 48
Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
1 5 10 15

acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag 96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
20 25 30

caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat 144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
35 40 45

gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg 192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
50 55 60

ggg agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag 240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
65 70 75 80

aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt 288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
85 90 95

cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg 336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
100 105 110

gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag 384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
115 120 125

tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg 432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
130 135 140

gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag 480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
145 150 155 160

ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga 528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
165 170 175

aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt 576
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
180 185 190

cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc 624
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
195 200 205

gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga 672
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
210 215 220

gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac 720
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
225 230 235 240

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caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc   768
Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
                245                250                255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca   816
Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
                260                265                270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc   864
Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
                275                280                285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa   912
Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
                290                295                300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc   960
Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
                305                310                315                320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg
1010
Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
                325                330

aat
1013

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<210> 524  
 <211> 330  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 524
Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
 1                5                10                15

Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
                20                25                30

Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35                40                45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50                55                60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
 65                70                75                80

Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
 85                90                95

Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
100                105                110

Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
115                120                125

Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
130                135                140

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Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
 145 150 155 160  
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
 165 170 175  
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
 180 185 190  
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
 210 215 220  
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
 225 230 235 240  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
 245 250 255  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
 260 265 270  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
 275 280 285  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
 290 295 300  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
 305 310 315 320  
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
 325 330

<210> 525  
 <211> 706  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(706)  
 <223> RXA01352

<400> 525  
 gtgcccaatg cattgggctg agattgcgcg ctgttgctgc gcgggaccgt tcgaacctgt 60  
 ctggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115  
 Val Phe Glu Asn Arg  
 1 5  
 ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163  
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu  
 10 15 20  
 gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211  
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca			259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala			
40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg			307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val			
55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga			355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly			
70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt			403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu			
90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act			451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr			
105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg			499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu			
120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca			547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser			
135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg			595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu			
150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg			643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val			
170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct			691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala			
185	190	195	
ttt tct gaa tct gat			706
Phe Ser Glu Ser Asp			
200			

&lt;210&gt; 526

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

Val Phe Glu Asn Arg Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala
1 5 10 15

Gly Ser Val Asp Glu Val Val His Thr Ala Ser Ala Ala Ala Arg Gly
20 25 30

Gly Ala Gly Val Val Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala
35 40 45

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser  
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser  
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp  
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile  
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu  
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr  
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro  
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val  
 165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val  
 180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp  
 195 200

&lt;210&gt; 527

&lt;211&gt; 944

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(921)

&lt;223&gt; RXA01381

&lt;400&gt; 527

tcc gca ggc gtt gga acc atc acg gtc atc gat gac gac acc gtc gac	48
Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp	
1 5 10 15	
att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt	96
Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly	
20 25 30	
cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca	144
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro	
35 40 45	
gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc	192
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala	
50 55 60	
tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct	240
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser	



65	70	75	80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act				288
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr				
	85	90	95	
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc				336
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu				
	100	105	110	
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc				384
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe				
	115	120	125	
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt				432
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly				
	130	135	140	
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac				480
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His				
	145	150	155	160
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc				528
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile				
	165	170	175	
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc				576
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser				
	180	185	190	
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag				624
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu				
	195	200	205	
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc				672
Ala Ala Arg Thr Asp Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly				
	210	215	220	
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa				720
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys				
	225	230	235	240
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc				768
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile				
	245	250	255	
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac				816
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp				
	260	265	270	
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac				864
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp				
	275	280	285	
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc				912
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val				
	290	295	300	
aac gcg ctg tagctgtcaa tttaagaggc cag				944
Asn Ala Leu				
305				

&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp  
 1 5 10 15

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
 20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
 35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
 50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser  
 65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr  
 85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu  
 100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe  
 115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly  
 130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His  
 145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile  
 165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser  
 180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu  
 195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly  
 210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys  
 225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile  
 245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp  
 260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp  
 275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val  
 290 295 300

Asn Ala Leu  
 305

<210> 529

<211> 259

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(259)

<223> RXA01360

<400> 529

gtggcaatca acgccgcggt cgtacccaga tcccagtggt cacgcgccat ttgtgacaac 60

gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115  
 Met Leu His Ile Ala  
 1 5

gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163  
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr  
 10 15 20

tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211  
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu  
 25 30 35

acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259  
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu  
 40 45 50

<210> 530

<211> 53

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 530

Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly  
 1 5 10 15

Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala  
 20 25 30

Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr  
 35 40 45

Thr Ser Ser Gly Glu  
 50

<210> 531

<211> 629

<212> DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(606)

&lt;223&gt; RXA01361

&lt;400&gt; 531

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gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg   48
Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
  1             5             10             15

acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg   96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
             20             25             30

gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg   144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
             35             40             45

aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc   192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
             50             55             60

gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt   240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
             65             70             75             80

gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc   288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
             85             90             95

gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc   336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
             100            105            110

gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att   384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
             115            120            125

gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc   432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
             130            135            140

ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg   480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
             145            150            155            160

tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca   528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
             165            170            175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt   576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
             180            185            190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga   626
Asp Val Cys Asp Pro Phe Arg His Gln Ile
             195            200

tta                                                                    629

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<210> 532  
 <211> 202  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 532  
 Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val  
     1                    5                    10                    15  
 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu  
                     20                    25                    30  
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala  
                     35                    40                    45  
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg  
                     50                    55                    60  
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe  
     65                    70                    75                    80  
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu  
                     85                    90                    95  
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly  
                     100                    105                    110  
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile  
                     115                    120                    125  
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr  
     130                    135                    140  
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala  
     145                    150                    155                    160  
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
                     165                    170                    175  
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
                     180                    185                    190  
 Asp Val Cys Asp Pro Phe Arg His Gln Ile  
     195                    200

<210> 533  
 <211> 927  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(904)  
 <223> RXA01208

<400> 533  
 tactaggcac ggggtgccaa ccggatggaa aaattccgga ggctgagaaa acaccggttg 60  
 aacctgctct agctcgctact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

											Val	Ala	Asn	Ser	Phe	
											1				5	
ttg	gat	tct	tta	act	ctt	gtt	cga	caa	aac	act	ccc	ctt	gtt	cag	tgt	163
Leu	Asp	Ser	Leu	Thr	Leu	Val	Arg	Gln	Asn	Thr	Pro	Leu	Val	Gln	Cys	
				10					15					20		
ttg	acc	aac	tct	gtg	gtc	atg	caa	ttc	acg	gcc	aat	gtg	ttg	ctt	gcc	211
Leu	Thr	Asn	Ser	Val	Val	Met	Gln	Phe	Thr	Ala	Asn	Val	Leu	Leu	Ala	
				25					30					35		
gcg	ggt	gcg	acc	cct	gcg	atg	gtg	gat	act	cca	gct	gaa	tcg	gca	gaa	259
Ala	Gly	Ala	Thr	Pro	Ala	Met	Val	Asp	Thr	Pro	Ala	Glu	Ser	Ala	Glu	
		40					45					50				
ttc	gcc	gct	gtg	gcc	aat	gga	gtg	ctc	atc	aat	gcg	gga	act	cct	tct	307
Phe	Ala	Ala	Val	Ala	Asn	Gly	Val	Leu	Ile	Asn	Ala	Gly	Thr	Pro	Ser	
		55					60					65				
gcg	gag	caa	tac	caa	ggc	atg	acc	aag	gcc	att	gag	ggt	gca	cga	aaa	355
Ala	Glu	Gln	Tyr	Gln	Gly	Met	Thr	Lys	Ala	Ile	Glu	Gly	Ala	Arg	Lys	
70					75					80					85	
gct	ggc	aca	cca	tgg	gtg	tta	gac	cca	gtt	gct	gtg	ggt	ggg	ttg	tcg	403
Ala	Gly	Thr	Pro	Trp	Val	Leu	Asp	Pro	Val	Ala	Val	Gly	Gly	Leu	Ser	
				90					95					100		
gag	agg	acc	aag	tat	gcg	gag	gga	atc	gtc	gat	aag	cag	cct	gcc	gca	451
Glu	Arg	Thr	Lys	Tyr	Ala	Glu	Gly	Ile	Val	Asp	Lys	Gln	Pro	Ala	Ala	
			105					110					115			
att	cgt	gga	aac	gcc	tca	gag	gtc	gtg	gcg	ctt	gcg	ggg	ctc	ggt	gcc	499
Ile	Arg	Gly	Asn	Ala	Ser	Glu	Val	Val	Ala	Leu	Ala	Gly	Leu	Gly	Ala	
		120					125					130				
ggt	ggg	cgc	ggc	gta	gac	gcg	acc	gat	tcc	gtg	gaa	gtg	gcg	ttg	gag	547
Gly	Gly	Arg	Gly	Val	Asp	Ala	Thr	Asp	Ser	Val	Glu	Val	Ala	Leu	Glu	
		135					140					145				
gcg	gcg	caa	ttg	ttg	gcc	aag	cgc	act	ggt	ggc	gtc	gtg	gct	gtc	tct	595
Ala	Ala	Gln	Leu	Leu	Ala	Lys	Arg	Thr	Gly	Gly	Val	Val	Ala	Val	Ser	
150					155					160					165	
ggt	gcg	gag	gac	ttg	att	gtg	tct	gcg	gat	cgg	gtg	acg	tgg	ttg	cgt	643
Gly	Ala	Glu	Asp	Leu	Ile	Val	Ser	Ala	Asp	Arg	Val	Thr	Trp	Leu	Arg	
				170					175					180		
tcg	ggg	gat	ccg	atg	ttg	cag	ctg	gtg	att	ggc	act	gga	tgc	tct	ttg	691
Ser	Gly	Asp	Pro	Met	Leu	Gln	Leu	Val	Ile	Gly	Thr	Gly	Cys	Ser	Leu	
			185					190					195			
ggc	gcg	ctg	aca	gct	gca	tat	cta	ggc	gcc	acg	gtt	gac	tca	gat	att	739
Gly	Ala	Leu	Thr	Ala	Ala	Tyr	Leu	Gly	Ala	Thr	Val	Asp	Ser	Asp	Ile	
		200					205					210				
tcc	gcg	cac	gat	gct	gtg	ttg	gct	gcg	cat	gcc	cat	gtg	ggt	gct	gct	787
Ser	Ala	His	Asp	Ala	Val	Leu	Ala	Ala	His	Ala	His	Val	Gly	Ala	Ala	
		215					220					225				
ggc	cag	att	gca	gca	cag	aag										

230	235	240	245	
gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg	883			
Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser				
250	255	260		
ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt	927			
Leu Val Asp Val Arg Glu Ala				
265				

&lt;210&gt; 534

&lt;211&gt; 268

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 534

Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr	
1 5 10 15	
Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala	
20 25 30	
Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro	
35 40 45	
Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn	
50 55 60	
Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile	
65 70 75 80	
Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala	
85 90 95	
Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp	
100 105 110	
Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu	
115 120 125	
Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val	
130 135 140	
Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly	
145 150 155 160	
Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg	
165 170 175	
Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly	
180 185 190	
Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr	
195 200 205	
Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala	
210 215 220	
His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro	
225 230 235 240	

Gly Ser Phe Ala Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala  
 245 250 255

Gln Ala Val Ala Ser Leu Val Asp Val Arg Glu Ala  
 260 265

<210> 535

<211> 1023

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1000)

<223> RXA00838

<400> 535

tcgtctaata gtgctgccaa tccaccggcc attgatgact cctttgtaga gaaggggtag 60

tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115  
 Met Lys Ile Ala Ile  
 1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu  
 10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211  
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala  
 25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259  
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr  
 40 45 50

gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307  
 Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp  
 55 60 65

gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct 355  
 Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala  
 70 75 80 85

gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403  
 Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln  
 90 95 100

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451  
 Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp  
 105 110 115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499  
 Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro  
 120 125 130

gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547  
 Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp  
 135 140 145



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tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg
1023
Lys Glu Glu Glu Asn Ser Leu
295 300

```

&lt;210&gt; 536

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 536

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Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
 1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

```

```

65              70              75              80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
      85              90              95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
      100             105             110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
      115             120             125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
      130             135             140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
      145             150             155             160
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
      165             170             175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
      180             185             190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
      195             200             205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
      210             215             220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
      225             230             235             240
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
      245             250             255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg
      260             265             270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr
      275             280             285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu
      290             295             300

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&lt;210&gt; 537

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02400

&lt;400&gt; 537

aggtgcccc aacgttgccct gttgactgca aattttccga aagaatccat aaactacttc 60

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ttaaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115
              Met Ser Ile Ser Arg
              1              5

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acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
      10                      15                      20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
      25                      30                      35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
      40                      45                      50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
      55                      60                      65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
      70                      75                      80                      85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
      90                      95                      100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
      105                      110                      115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
      120                      125                      130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
      135                      140                      145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
      150                      155                      160                      165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
      170                      175                      180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
Glu Val Pro Val Thr Phe Ala Ala Ala
      185                      190

tca 693

```

&lt;210&gt; 538

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 538

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Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu
  1           5           10           15

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Ser	Ala	Ala	Leu	Val	Ala	Cys	Ser	Pro	Pro	His	Gln	Gln	Asp	Ser	Pro
			20					25					30		
Val	Gln	Arg	Thr	Asn	Glu	Ile	Leu	Thr	Thr	Ser	Gln	Asn	Pro	Thr	Ser
		35					40					45			
Ala	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ala	Thr	Thr	Thr	Ser	Ser	Ala	Pro
	50					55					60				
Val	Glu	Glu	Asp	Val	Glu	Ile	Val	Val	Ser	Pro	Ala	Ala	Leu	Val	Asp
65					70					75					80
Gly	Glu	Gln	Val	Thr	Phe	Glu	Ile	Ser	Gly	Leu	Asp	Pro	Glu	Gly	Gly
				85					90					95	
Tyr	Tyr	Ala	Ala	Ile	Cys	Asp	Ser	Val	Ala	Asn	Pro	Gly	Asn	Pro	Val
			100					105					110		
Pro	Ser	Cys	Thr	Gly	Glu	Met	Ala	Asp	Phe	Thr	Ser	Gln	Ala	Trp	Leu
		115					120					125			
Ser	Asn	Ser	Gln	Pro	Gly	Ala	Thr	Val	Glu	Ile	Ala	Glu	Asp	Gly	Thr
	130					135					140				
Ala	Thr	Val	Glu	Leu	Glu	Ala	Thr	Ala	Thr	Gly	Thr	Gly	Leu	Asp	Cys
145					150					155					160
Thr	Thr	Gln	Ala	Cys	Val	Ala	Lys	Val	Phe	Gly	Asp	His	Thr	Glu	Gly
				165					170					175	
Phe	Arg	Asp	Val	Ala	Glu	Val	Pro	Val	Thr	Phe	Ala	Ala	Ala		
			180					185					190		

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<210> 539
<211> 1528
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1528)
<223> RXN01209
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<400> 539
cagattgcag cacagaaggc atcggcgcca ggcagctttg cgggtggcggtt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115
                                         Met Cys Glu Arg Pro
                                         1                               5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
                        10                               15                               20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
                        25                               30                               35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val

```

40	45	50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct			307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala			
55	60	65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag			355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu			
70	75	80	85
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa			403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln			
	90	95	100
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa			451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu			
	105	110	115
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt			499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly			
	120	125	130
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg			547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala			
	135	140	145
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag			595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu			
150	155	160	165
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga			643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly			
	170	175	180
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac			691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp			
	185	190	195
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct			739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala			
	200	205	210
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa			787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu			
	215	220	225
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat			835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn			
230	235	240	245
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca			883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr			
	250	255	260
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc			931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly			
	265	270	275
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac			979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His			
	280	285	290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

gcc gcc ggc gaa agc gtg gaa  
 1528  
 Ala Ala Gly Glu Ser Val Glu  
 470 475

&lt;210&gt; 540

&lt;211&gt; 476

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 540

```

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
  1              5              10              15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
      20              25              30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
      35              40              45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
      50              55              60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
      65              70              75              80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
      85              90              95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
      100             105             110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
      115             120             125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
      130             135             140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
      145             150             155             160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
      165             170             175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
      180             185             190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
      195             200             205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
      210             215             220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
      225             230             235             240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
      245             250             255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
      260             265             270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
      275             280             285

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Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu  
 465 470 475

&lt;210&gt; 541

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; FRXA01209

&lt;400&gt; 541

cagattgcag cacagaaggc atcggcgcca ggcagctttg cggtggcggtt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
 Met Cys Glu Arg Pro  
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
 25 30 35



tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag gcc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggg ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggg ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	

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ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac   979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
      280                      285                      290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
1027
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
      295                      300                      305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
1075
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
310                      315                      320                      325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
1123
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
      330                      335                      340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
1171
Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
      345                      350                      355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
1219
Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
      360                      365                      370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
1267
Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
      375                      380                      385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
1315
Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
390                      395                      400                      405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
1363
Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
      410                      415                      420

ggg gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
1411
Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
      425                      430                      435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
1459
Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
      440                      445                      450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
1507
Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
      455                      460                      465

gcc gcc ggc gaa agc gtg gaa
1528

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Ala Ala Gly Glu Ser Val Glu  
470 475

<210> 542

<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 542

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
260 265 270

Ile	Ala	Ala	Gly	Gly	Gly	Tyr	Gly	Met	Cys	Val	Val	Thr	Ser	Leu	Val
	275						280					285			
Ala	Gln	Asn	Thr	His	Gly	Val	Asn	Thr	Ile	His	Thr	Pro	Pro	Leu	Thr
	290					295					300				
Phe	Leu	Glu	Glu	Gln	Leu	Glu	Ala	Val	Phe	Ser	Asp	Val	Thr	Val	Asp
305					310					315					320
Ala	Ile	Lys	Leu	Gly	Met	Leu	Gly	Ser	Ala	Asp	Thr	Val	Asp	Leu	Val
				325					330					335	
Ala	Ser	Trp	Leu	Gly	Ser	His	Glu	His	Gly	Pro	Val	Val	Leu	Asp	Pro
			340					345					350		
Val	Met	Ile	Ala	Thr	Ser	Gly	Asp	Arg	Leu	Leu	Asp	Ala	Ser	Ala	Glu
	355						360					365			
Glu	Ser	Leu	Arg	Arg	Leu	Ala	Val	His	Val	Asp	Val	Val	Thr	Pro	Asn
	370					375					380				
Ile	Pro	Glu	Leu	Ala	Val	Leu	Cys	Asp	Ser	Ala	Pro	Ala	Ile	Thr	Met
385					390					395					400
Asp	Glu	Ala	Ile	Ala	Gln	Ala	Gln	Gly	Phe	Ala	Arg	Thr	His	Asp	Thr
				405					410					415	
Ile	Val	Ile	Val	Lys	Gly	Gly	His	Leu	Thr	Gly	Ala	Leu	Ala	Asp	Asn
			420					425					430		
Ala	Val	Val	Arg	Pro	Asp	Gly	Ser	Val	Phe	Gln	Val	Glu	Asn	Leu	Arg
		435					440					445			
Val	Asn	Thr	Thr	Asn	Ser	His	Gly	Thr	Gly	Cys	Ser	Leu	Ser	Ala	Ser
	450					455					460				
Leu	Ala	Thr	Lys	Ile	Ala	Ala	Gly	Glu	Ser	Val	Glu				
465					470					475					

<210> 543

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

**<220>**

<221> CDS

<222> (101) .. (700)

<223> RXN01413

<400> 543

tttgccctat tggaagaagt aaattccaca ccttcacttt ccaatacttc ttttggtgag 60

cgggtttctt cagcgtttta ccatctgaaa ccatctgaga ttg acc cat ctg ttc 115  
 Leu Thr His Leu Phe  
 1 5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163  
Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr  
10 15 20

```

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
      25                      30                      35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
      40                      45                      50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
      55                      60                      65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
      70                      75                      80                      85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
      90                      95                      100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
      105                      110                      115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
      120                      125                      130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
      135                      140                      145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
      150                      155                      160                      165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
      170                      175                      180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
      185                      190                      195

gac aac aag tagagtttta aaataccgat caa 723
Asp Asn Lys
      200

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&lt;210&gt; 544

&lt;211&gt; 200

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 544

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Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
 1              5              10              15

```

```

Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
      20              25              30

```

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<210> 545
<211> 795
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(772)  
<223> RXN01617
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784

40	45	50	
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc			307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
55	60	65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc			355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
	90	95	100
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
	105	110	115
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
	120	125	130
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
	135	140	145
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
	170	175	180
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
	185	190	195
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
	200	205	210
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
	215	220	
cct			795
<210> 546			
<211> 224			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 546			
Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala			
1	5	10	15
Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu			
	20	25	30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
           35                          40                          45  
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
           50                          55                          60  
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
           65                          70                          75                          80  
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr  
                           85                          90                          95  
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu  
                           100                          105                          110  
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly  
           115                          120                          125  
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn  
           130                          135                          140  
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu  
           145                          150                          155                          160  
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala  
                           165                          170                          175  
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala  
           180                          185                          190  
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val  
           195                          200                          205  
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
           210                          215                          220

&lt;210&gt; 547

&lt;211&gt; 638

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (615)

&lt;223&gt; FRXA01617

&lt;400&gt; 547

gct aat cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg 48  
 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
       1                          5                          10                          15  
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96  
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
           20                          25                          30  
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144  
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu



35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
85	90	95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
115	120	125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
130	135	140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
165	170	175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
180	185	190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
195	200	205	
aaacaagctc cct			638

&lt;210&gt; 548

&lt;211&gt; 205

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 548

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val	
1	15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr	
20	30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu	
35	45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala	
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50	55	60
Leu Arg Ala Lys Val	Leu Pro Gln Ala Thr	Val Val Thr Pro Asn Asn
65	70	75 80
Phe Glu Ala Thr	Thr Leu Ser Gly Leu	Asp Lys Leu Glu Thr Ile Asp
	85	90 95
Asp Leu Lys Glu	Ala Ala Arg Leu Ile His	Glu Gln Gly Pro Gln Tyr
	100	105 110
Val Val Val Lys	Gly Gly Ile Asp Phe Pro	Gly Asp Asn Ala Val Asp
	115	120 125
Val Leu Phe Asp	Gly Thr Asp Tyr His Val	Phe Ser Glu Pro Lys Ile
	130	135 140
Gly Asp Glu Arg	Val Ser Gly Ala Gly Cys	Thr Phe Ala Ala Val Ile
	145	150 155 160
Thr Ala Glu Leu	Ala Lys Gly Asn Ser	Ala Val Asp Ala Val Thr Thr
	165	170 175
Ala Lys Arg Val	Val Thr Arg Ala Val	Lys Asp Ala Val Ala Ser Asn
	180	185 190
Ala Pro Phe Thr	Ser Val Trp Leu Ala Glu	Asp Asn Lys
	195	200 205

&lt;210&gt; 549

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(892)

&lt;223&gt; RXS01807

&lt;400&gt; 549

gctcaccgag ctggacacca agctccgcgc agtgcaggaa gaacacggcg agctggaaat 60

gcagtggctg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc 115  
 Met Pro Ser Ala Gly  
 1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163  
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg  
 10 15 20

gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211  
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
 25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259  
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val  
 40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307  
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac			355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp			
70	75	80	85
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc			403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly			
	90	95	100
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag			451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln			
	105	110	115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc			499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile			
	120	125	130
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc			547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr			
	135	140	145
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat			595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn			
	150	155	160
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg			643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu			
	170	175	180
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act			691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr			
	185	190	195
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa			739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu			
	200	205	210
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc			787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val			
	215	220	225
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc			835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile			
	230	235	240
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc			883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr			
	250	255	260
aaa gcg ctt taggtttcgt ccgtctctga cag			915
Lys Ala Leu			

&lt;210&gt; 550

&lt;211&gt; 264

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 550

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Met  Pro  Ser  Ala  Gly  Glu  Glu  Ile  Leu  Glu  Gln  Arg  Ala  Gln  Leu  Glu
 1              5              10              15

Phe  Asp  Gln  Arg  Arg  Ala  Asp  Val  Val  Met  Ile  Gly  Ser  Gln  Val  Val
              20              25              30

Tyr  Gly  Ser  Val  Gly  Leu  Ser  Ala  Ala  Ile  Pro  Val  Met  His  Asn  Glu
              35              40              45

Gly  Leu  Arg  Val  Val  Ala  Val  Pro  Thr  Val  Val  Leu  Ser  Ser  Met  Pro
 50              55              60

Arg  Tyr  Ala  Ser  Ser  His  Arg  Gln  Pro  Met  Ser  Asp  Gln  Trp  Leu  Ala
 65              70              75              80

Asp  Ala  Leu  Gln  Asp  Leu  Val  Asp  Leu  Gly  Ile  Ile  Asp  Glu  Val  Ser
              85              90              95

Thr  Ile  Ser  Thr  Gly  Tyr  Phe  Thr  Ser  Ala  Ser  Gln  Val  Arg  Val  Val
              100              105              110

Ala  Ala  Trp  Leu  Gln  Lys  Ile  Arg  Glu  Thr  His  Pro  His  Val  Arg  Ile
 115              120              125

Val  Val  Asp  Pro  Ile  Met  Gly  Asp  Ser  Asp  Val  Gly  Ile  Tyr  Val  Ala
 130              135              140

Asp  Glu  Ile  Ala  Thr  Ala  Ile  Cys  Gln  Asp  Leu  Cys  Pro  Leu  Ala  Thr
 145              150              155              160

Gly  Ile  Ile  Pro  Asn  Ala  Phe  Glu  Leu  Ser  His  Met  Val  Gly  Ser  Gly
              165              170              175

Asp  Pro  Arg  Ser  Leu  Leu  Gly  Pro  Phe  Gly  Glu  Trp  Ile  Ile  Ile  Thr
              180              185              190

Ser  Ala  Thr  Glu  Thr  Val  Gly  Thr  Thr  Val  Thr  Arg  Ile  Val  Thr  Arg
 195              200              205

Asp  Ser  Val  Gln  Glu  Ile  Ala  Ser  Ala  Thr  Val  Asp  Thr  Thr  Ala  Lys
 210              215              220

Gly  Ala  Gly  Asp  Val  Tyr  Ala  Ala  Ala  Leu  Ile  Ala  Ala  Leu  His  Lys
 225              230              235              240

Asp  Phe  Ser  Leu  Ile  Asp  Ala  Ala  Ser  His  Ala  Ser  Asn  Thr  Val  Cys
              245              250              255

Ala  Gly  Leu  Gln  Thr  Lys  Ala  Leu
              260

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&lt;210&gt; 551

&lt;211&gt; 622

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(622)

&lt;223&gt; RXC01021

&lt;400&gt; 551

cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115  
Met Ser Ser Ser Glu  
1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163  
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu  
10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211  
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala  
25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259  
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala  
40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307  
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val  
55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355  
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met  
70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403  
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val  
90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451  
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg  
105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499  
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln  
120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547  
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu  
135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595  
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu  
150 155 160 165

ggc act gtt gtc act gtg ttg cgt tct 622  
Gly Thr Val Val Thr Val Leu Arg Ser  
170

&lt;210&gt; 552

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 552

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro  
1 5 10 15

Ser	Val	Gln	Pro 20	Glu	Arg	Arg	Ala	Asp 25	Ser	Thr	Gly	Ala	Pro 30	Ala	Ala
Ala	Ser	Lys 35	Glu	Ala	Ser	Gln	Gln 40	Met	Asp	Ala	Ala	Gly 45	Val	Leu	Glu
Trp	Ala 50	Arg	Thr	Ala	Val	Glu 55	Gln	Leu	Ser	Glu	Arg 60	Arg	Ala	Glu	Ile
Asn 65	Ala	Leu	Asn	Val	Phe 70	Pro	Val	Pro	Asp	Ala 75	Asp	Thr	Gly	Ser	Asn 80
Met	Thr	Tyr	Thr	Met 85	Thr	Ala	Ala	Leu	Asp 90	Glu	Ala	Leu	Lys	Leu 95	Gly
Glu	Leu	Gly	Asp 100	Val	Ala	Arg	Ile 105	Thr	Glu	Ala	Leu	Ala	Val 110	Gly	Ser
Val	Arg	Gly 115	Ala	Arg	Gly	Asn	Ser 120	Gly	Val	Val	Leu	Ser 125	Gln	Val	Leu
Arg 130	Ala	Ile	Ala	Gln	Ala	Ala 135	Ala	Asp	Gly	Val	Ile 140	Asp	Gly	His	Thr
Ile 145	Gln	Glu	Ala	Leu	Ser 150	Ile	Ala	Arg	Ser	Leu 155	Val	Asp	Arg	Ala	Ile 160
Thr	Asp	Pro	Val	Glu 165	Gly	Thr	Val	Val 170	Thr	Val	Leu	Arg	Ser		

<210> 553

<211> 1107

<212> DNA

<213> *Corynebacterium glutamicum*

**<220>**

<221> CDS

<222> (101) .. (1084)

<223> RXN02246

<400> 553

tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60

caacaaggcg atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac 115  
Met Asp Val Ala His  
1 5

gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163  
Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
10 15 20

agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211  
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu  
 25 30 35

gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259  
Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu  
40 45 50

gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg	307
Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala	
55 60 65	
gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt	355
Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys	
70 75 80 85	
tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc  
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr  
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga  
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg  
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga  
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
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Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
195 200 205



Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
 210 215 220  
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
 225 230 235 240  
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
 245 250 255  
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
 260 265 270  
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
 275 280 285  
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
 290 295 300  
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
 305 310 315 320  
 Ile Glu Met Met Arg Lys Glu His  
 325

<210> 555  
 <211> 1107  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1084)  
 <223> FRXA02246

<400> 555  
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 caacaaggcg atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac 115  
 Met Asp Val Ala His  
 1 5  
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163  
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
 10 15 20  
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211  
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu  
 25 30 35  
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259  
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu  
 40 45 50  
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307  
 Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala  
 55 60 65  
 gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355  
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys  
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	
aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc	1027
Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr	
295 300 305	
acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga	1075
Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg	

310                                      315                                      320                                      325  
 aag gaa cac taaatgttca caggtattgt cga  
 1107  
 Lys Glu His  
  
 <210> 556  
 <211> 328  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 556  
 Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
   1                                  5                                  10                                  15  
 Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
                                   20                                  25                                  30  
 Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
                                   35                                  40                                  45  
 Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
   50                                  55                                  60  
 Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
   65                                  70                                  75                                  80  
 Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
                                   85                                  90                                  95  
 Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
                                   100                                  105                                  110  
 Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
   115                                  120                                  125  
 Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
   130                                  135                                  140  
 His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
   145                                  150                                  155                                  160  
 Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
                                   165                                  170                                  175  
 Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
                                   180                                  185                                  190  
 Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
   195                                  200                                  205  
 Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
   210                                  215                                  220  
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
   225                                  230                                  235                                  240  
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
                                   245                                  250                                  255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
                   260                                  265                                  270  
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
                   275                                  280                                  285  
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
                   290                                  295                                  300  
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
 305                                  310                                  315                                  320  
 Ile Glu Met Met Arg Lys Glu His  
                                   325

&lt;210&gt; 557

&lt;211&gt; 756

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(733)

&lt;223&gt; RXA02247

&lt;400&gt; 557

acaagaaacc acgatggatc agattatgcg ttttgacacc acgtccgtga gacagttggg 60

ttcagatgta ttgatagaaa tgatgagaaa ggaacactaa atg ttc aca ggt att 115  
   Met Phe Thr Gly Ile  
   1                                  5

gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163  
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser  
                                   10                                  15                                  20

atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211  
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu  
                                   25                                  30                                  35

ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259  
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe  
                                   40                                  45                                  50

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307  
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg  
                                   55                                  60                                  65

agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355  
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg  
                                   70                                  75                                  80                                  85

gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403  
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His  
                                   90                                  95                                  100

gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451  
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp  
                                   105                                  110                                  115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499  
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val  
120 125 130  
  
gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547  
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser  
135 140 145  
  
ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595  
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg  
150 155 160 165  
  
gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643  
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu  
170 175 180  
  
gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691  
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
185 190 195  
  
gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733  
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp  
200 205 210  
  
taggttagac aacgtgagtg aac 756

&lt;210&gt; 558

&lt;211&gt; 211

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 558

Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu  
1 5 10 15  
  
His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu  
20 25 30  
  
Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu  
35 40 45  
  
Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln  
50 55 60  
  
Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys  
65 70 75 80  
  
Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His  
85 90 95  
  
Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr  
100 105 110  
  
Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu  
115 120 125  
  
Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser  
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile  
 145 150 155 160  
 Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp  
 165 170 175  
 Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met  
 180 185 190  
 Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe  
 195 200 205  
 Thr Arg Asp  
 210

<210> 559  
 <211> 1389  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1366)  
 <223> RXN02248

<400> 559  
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 aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115  
 Val Ser Glu His Glu  
 1 5  
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163  
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile  
 10 15 20  
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211  
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn  
 25 30 35  
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val  
 40 45 50  
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307  
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr  
 55 60 65  
 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355  
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn  
 70 75 80 85  
 cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403  
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr  
 90 95 100  
 ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451  
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499  
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His  
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547  
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly  
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595  
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro  
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643  
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met  
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691  
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys  
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739  
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile  
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787  
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr  
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835  
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val  
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883  
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu  
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931  
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg  
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979  
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln  
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga  
 1027  
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg  
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa  
 1075  
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu  
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat  
 1123  
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp  
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg  
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val  
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt  
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu  
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct  
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala  
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg  
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met  
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa  
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu  
 410 415 420

aac taaggagcac aacaatggct aaa  
 1389  
 Asn

<210> 560  
 <211> 422  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 560  
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 20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
 130 135 140



Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
 145 150 155 160  
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
 165 170 175  
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
 180 185 190  
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
 195 200 205  
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
 210 215 220  
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
 225 230 235 240  
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
 245 250 255  
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
 420

&lt;210&gt; 561

&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1366)

&lt;223&gt; FRXA02248

&lt;400&gt; 561

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aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
                                         Val Ser Glu His Glu
                                         1      5
cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
              10              15              20
gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
              25              30              35
gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
              40              45              50
gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
              55              60              65
gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
              70              75              80              85
cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
              90              95              100
ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
              105              110              115
ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
              120              125              130
gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
              135              140              145
cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
              150              155              160              165
gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
              170              175              180
gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
              185              190              195
ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739

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Leu	Ile	Ser	Ile	Glu	Gln	Leu	Ile	Glu	Trp	Arg	Arg	Lys	Asn	Glu	Ile		
		200					205					210					
ttg	gtg	gag	cgc	cag	gtg	gaa	act	gtg	ctg	cct	acc	gat	ttc	ggc	acg	787	
Leu	Val	Glu	Arg	Gln	Val	Glu	Thr	Val	Leu	Pro	Thr	Asp	Phe	Gly	Thr		
	215					220					225						
ttc	aag	gct	gtt	ggc	tac	cgt	tcc	atc	atc	gat	ggc	acc	gag	ctt	gtt	835	
Phe	Lys	Ala	Val	Gly	Tyr	Arg	Ser	Ile	Ile	Asp	Gly	Thr	Glu	Leu	Val		
230					235					240					245		
gcc	att	gtt	gcc	ggc	gac	gtg	gca	tcc	gac	ggc	ggc	gaa	aac	gtc	ctg	883	
Ala	Ile	Val	Ala	Gly	Asp	Val	Ala	Ser	Asp	Gly	Gly	Glu	Asn	Val	Leu		
				250					255					260			
gtt	cga	gtc	cac	tct	gag	tgc	ttg	act	ggc	gat	gtt	ttt	gga	tcc	cgg	931	
Val	Arg	Val	His	Ser	Glu	Cys	Leu	Thr	Gly	Asp	Val	Phe	Gly	Ser	Arg		
			265					270					275				
cgc	tgc	gac	tgt	gga	cag	cag	ctg	cac	gag	tct	ttg	cgc	ctg	atc	cag	979	
Arg	Cys	Asp	Cys	Gly	Gln	Gln	Leu	His	Glu	Ser	Leu	Arg	Leu	Ile	Gln		
		280					285					290					
gaa	gct	ggc	cgg	gga	gta	gtg	gtg	tac	atg	cgt	ggg	cat	gag	gga	cga		
1027																	
Glu	Ala	Gly	Arg	Gly	Val	Val	Val	Tyr	Met	Arg	Gly	His	Glu	Gly	Arg		
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ggc	att	ggc	ctg	ctc	gcc	aag	cta	cgc	gcc	tac	caa	ctc	cag	gat	gaa		
1075																	
Gly	Ile	Gly	Leu	Leu	Ala	Lys	Leu	Arg	Ala	Tyr	Gln	Leu	Gln	Asp	Glu		
310					315				320					325			
ggc	gcc	gac	acc	gtc	gat	gcc	aac	ctc	gca	ctt	ggc	ctt	cca	gcc	gat		
1123																	
Gly	Ala	Asp	Thr	Val	Asp	Ala	Asn	Leu	Ala	Leu	Gly	Leu	Pro	Ala	Asp		
				330					335					340			
gcc	cgc	gaa	ttt	ggc	acc	agc	gcc	cag	att	ctc	tac	gac	ttg	ggc	gtg		
1171																	
Ala	Arg	Glu	Phe	Gly	Thr	Ser	Ala	Gln	Ile	Leu	Tyr	Asp	Leu	Gly	Val		
			345					350					355				
cgc	tcg	ctc	aac	ttg	atc	agc	aac	aac	cca	gcc	aag	aag	gtg	gga	ctt		
1219																	
Arg	Ser	Leu	Asn	Leu	Ile	Ser	Asn	Asn	Pro	Ala	Lys	Lys	Val	Gly	Leu		
		360					365					370					
gaa	ggc	cac	ggc	att	tcc	att	gcc	agc	cga	acc	ccc	atc	cct	gtt	gct		
1267																	
Glu	Gly	His	Gly	Ile	Ser	Ile	Ala	Ser	Arg	Thr	Pro	Ile	Pro	Val	Ala		
	375					380					385						
gtt	cat	gaa	gac	aat	gtt	cga	tac	ctg	aaa	acc	aag	cgt	gac	cgc	atg		
1315																	
Val	His	Glu	Asp	Asn	Val	Arg	Tyr	Leu	Lys	Thr	Lys	Arg	Asp	Arg	Met		
390				395					400						405		
gga	cat	gac	ctc	cca	gat	gtc	gca	ctg	tgg	gaa	caa	gag	cac	cca	gaa		
1363																	
Gly	His	Asp	Leu	Pro	Asp	Val	Ala	Leu	Trp	Glu	Gln	Glu	His	Pro	Glu		

410 415 420

aac taaggagcac aacaatggct aaa  
1389  
Asn

<210> 562  
<211> 422  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 562  
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1 5 10 15  
Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp  
20 25 30  
Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
35 40 45  
Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
50 55 60  
Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
65 70 75 80  
Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
85 90 95  
Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
100 105 110  
His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
115 120 125  
Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
130 135 140  
Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
145 150 155 160  
Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
165 170 175  
Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
180 185 190  
Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
195 200 205  
Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
210 215 220  
Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
225 230 235 240  
Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
245 250 255

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<211> 600
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(577)
<223> RXN02249
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tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
                                         Met Ala Lys Glu Gly
                                         1                               5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
                        10                               15                               20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
                        25                               30                               35

gca gta gat gcg gga cgt gca gca gga gca acg qtg aqc gaa tac cgc 259

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Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu  
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597  
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
150 155

ttg 600

&lt;210&gt; 564

&lt;211&gt; 159

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 564

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly  
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp  
20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr  
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala  
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(577)

<223> FRXA02249

<400> 565

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tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115  
 Met Ala Lys Glu Gly  
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259  
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
 40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
 55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
 70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
 90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
 105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
 Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
 120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145  
 gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597  
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
 150 155

ttg 600

<210> 566

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 566

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly  
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp  
 20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr  
 35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
 50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
 65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
 85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
 100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala  
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
 145 150 155

<210> 567

<211> 702

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(679)

<223> RXA02250

<400> 567

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tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115  
 Val Thr Thr Asn Ala



	1	5	
ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc			163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val			
	10	15	20
ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc			211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr			
	25	30	35
gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg			259
Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Glu Leu Glu Val			
	40	45	50
acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc			307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile			
	55	60	65
atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc			355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr			
	70	75	80
ggg gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc			403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly			
	90	95	100
atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg			451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val			
	105	110	115
cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt			499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg			
	120	125	130
ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc			547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser			
	135	140	145
agc gtg gca cgt ttg gag ctt cca gac ttt gaa ttc gtt ccc atg tgg			595
Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp			
	150	155	160
gct ttc cag tcc cgc gat gga gaa gat gtg gtg cgc gcg gtt gcg acc			643
Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr			
	170	175	180
ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct			689
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp			
	185	190	
gtggctgatac caa			702

&lt;210&gt; 568

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 568

Val Thr Thr Asn Ala Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala
1 5 10 15

His	Ser	Gly	Ala	Val	Gly	Lys	Pro	Lys	Val	Gln	Leu	Ser	Asp	Ala	Glu	
			20					25					30			
Ile	Gln	Glu	Tyr	Thr	Ala	Ala	Phe	Ala	Gly	Thr	Thr	Thr	Thr	Lys	Pro	
			35				40				45					
Trp	Glu	Leu	Glu	Val	Thr	Thr	Lys	Phe	Leu	Lys	Lys	Ile	Ala	Trp	Val	
			50				55				60					
Ala	Val	Val	Val	Ile	Met	Ala	Val	His	Ile	Phe	Met	Gly	Ala	Val	Val	
			65				70				75					
Asp	Val	Asp	Phe	Thr	Gly	Ala	Ala	Val	Thr	Phe	Val	Asp	Thr	Leu	Ala	
				85				90					95			
Phe	Pro	Ala	Leu	Gly	Ile	Ile	Phe	Ser	Val	Leu	Val	Phe	Leu	Gly	Leu	
			100				105				110					
Thr	Arg	Pro	Arg	Val	Arg	Ala	Asn	Glu	Asp	Gly	Val	Glu	Val	Arg	Asn	
			115				120				125					
Phe	Ile	Gly	Thr	Arg	Phe	Tyr	Pro	Trp	Val	Val	Ile	Tyr	Gly	Met	Ser	
			130				135				140					
Phe	Pro	Lys	Gly	Ser	Ser	Val	Ala	Arg	Leu	Glu	Leu	Pro	Asp	Phe	Glu	
			145				150				155					
Phe	Val	Pro	Met	Trp	Ala	Phe	Gln	Ser	Arg	Asp	Gly	Glu	Asp	Val	Val	
				165				170					175			
Arg	Ala	Val	Ala	Thr	Phe	Arg	Asp	Leu	Glu	Asn	Lys	Tyr	Met	Pro	Glu	
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Asp

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<210> 569
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1123)
<223> RXA01489
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agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
Val Asp Ile Trp Ser
1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
10 15 20

ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

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25	30	35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr 40 45 50			259
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr 55 60 65			307
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly 70 75 80 85			355
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu 90 95 100			403
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala 105 110 115			451
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala 120 125 130			499
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn 135 140 145			547
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser 150 155 160 165			595
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn 170 175 180			643
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly 185 190 195			691
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr 200 205 210			739
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp 215 220 225			787
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp 230 235 240 245			835
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser 250 255 260			883
gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala 265 270 275			931

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979  
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val  
           280                                  285                                  290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac  
 1027  
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp  
           295                                  300                                  305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc  
 1075  
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile  
           310                                  315                                  320                                  325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct  
 1123  
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala  
                                   330                                  335                                  340

taaggccggt caccggccat caa  
 1146

<210> 570  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln  
                   20                                  25                                  30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro  
                   35                                  40                                  45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro  
           50                                  55                                  60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu  
           65                                  70                                  75                                  80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys  
                   85                                  90                                  95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val  
                   100                                  105                                  110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe  
           115                                  120                                  125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln  
           130                                  135                                  140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp  
           145                                  150                                  155                                  160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu

	165		170		175
Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly					
	180		185		190
Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro					
	195		200		205
Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly					
	210		215		220
Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys					
	225		230		235
Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr					
	245		250		255
Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg					
	260		265		270
Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly					
	275		280		285
His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys					
	290		295		300
Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr					
	305		310		315
Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp					
	325		330		335
Thr Gln Pro Ser Ala					
	340				

<210> 571  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1174)  
 <223> RXA02135

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aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag	115
Met Val Pro Ala Glu	
1 5	

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg	163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr	
10 15 20	

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag	211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys	
25 30 35	

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser  
           280                                  285                                  290  
 gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg  
 1027  
 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met  
           295                                  300                                  305  
 tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag  
 1075  
 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys  
 310                                  315                                  320                                  325  
 att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc  
 1123  
 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly  
                                   330                                  335                                  340  
 gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg  
 1171  
 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr  
                                   345                                  350                                  355  
 gag taactttcta agcgatgtcc ggc  
 1197  
 Glu

<210> 572  
 <211> 358  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 572  
 Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys  
       1                                  5                                  10                                  15  
 Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro  
                                   20                                  25                                  30  
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys  
                                   35                                  40                                  45  
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val  
                                   50                                  55                                  60  
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro  
                                   65                                  70                                  75                                  80  
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala  
                                   85                                  90                                  95  
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile  
                                   100                                  105                                  110  
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg  
                                   115                                  120                                  125  
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val  
                                   130                                  135                                  140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp  
 145 150 155 160  
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr  
 165 170 175  
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val  
 180 185 190  
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu  
 195 200 205  
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg  
 210 215 220  
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala  
 225 230 235 240  
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val  
 245 250 255  
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys  
 260 265 270  
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr  
 275 280 285  
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile  
 290 295 300  
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala  
 305 310 315 320  
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr  
 325 330 335  
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala  
 340 345 350  
 Pro Glu Gln Asn Thr Glu  
 355

&lt;210&gt; 573

&lt;211&gt; 1146

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1123)

&lt;223&gt; RXA01489

&lt;400&gt; 573

gtcatgggat gtcattccgg cgggcttgat gacgatcacg agtccaggtt taggggcagg 60

 agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115  
 Val Asp Ile Trp Ser

1 5



gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
25 30 35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc	259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883

Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser  
 250 255 260

gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca 931  
 Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala  
 265 270 275

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979  
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val  
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac  
 1027  
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp  
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc  
 1075  
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile  
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct  
 1123  
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala  
 330 335 340

taaggccggt caccggccat caa  
 1146

&lt;210&gt; 574

&lt;211&gt; 341

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 574

Val Asp Ile Trp Ser Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly  
 1 5 10 15

Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln  
 20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro  
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro  
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu  
 65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys  
 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val  
 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe  
 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln

130                      135                      140  
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp  
 145                      150                      155                      160  
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu  
                     165                      170                      175  
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly  
                     180                      185                      190  
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro  
                     195                      200                      205  
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly  
                     210                      215                      220  
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys  
 225                      230                      235                      240  
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr  
                     245                      250                      255  
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg  
                     260                      265                      270  
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly  
                     275                      280                      285  
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys  
                     290                      295                      300  
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr  
 305                      310                      315                      320  
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp  
                     325                      330                      335  
 Thr Gln Pro Ser Ala  
                     340

&lt;210&gt; 575

&lt;211&gt; 805

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (87)..(782)

&lt;223&gt; RXN01712

&lt;400&gt; 575

gccggccttag gtcctccga ccagaacccc actggcacct ttggataaca ccattccgtg 60

taaacaagct ggcctagact tgaaacatg gtc gat atc ttg gaa ctc atc ggt 113  
                     Met Val Asp Ile Leu Glu Leu Ile Gly  
                     1                      5

ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161  
 Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

10	15	20	25	
gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga				209
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile	110	115	120	
acg gat aat tcc gat caa gca aag cag cag ccg ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His	170	175	180	185
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys	220	225	230	
tgagtggttg actctccgga tct				805

&lt;210&gt; 576

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 576

Met Val Asp Ile Leu Glu Leu Ile Gly Pro Leu Pro Phe Val Ser Thr  
 1 5 10 15

Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr  
 20 25 30

Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu  
 35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser  
 50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile  
 65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala  
 85 90 95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu  
 100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala  
 115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu  
 130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr  
 145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu  
 165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu  
 180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro  
 195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu  
 210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys  
 225 230

&lt;210&gt; 577

&lt;211&gt; 578

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)..(555)

&lt;223&gt; FRXA01712

&lt;400&gt; 577

cttctgttgg cgcttcgcag gtggtcggac gtggtgttgg ttgggtcgag caccgtg 57  
 Val

1

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aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
      5              10              15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
      20              25              30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
      35              40              45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
      50              55              60              65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
      70              75              80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
      85              90              95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
      100              105              110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly
      115              120              125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
      130              135              140              145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu
      150              155              160

cgg tat aag cgc gcc aag tgagtgttgg actctccgga tct 578
Arg Tyr Lys Arg Ala Lys
      165

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&lt;210&gt; 578

&lt;211&gt; 167

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 578

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Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln
  1              5              10              15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val
      20              25              30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu
      35              40              45

```

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys  
50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr  
65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala  
85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala  
100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser  
115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg  
130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe  
145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys  
165

&lt;210&gt; 579

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(808)

&lt;223&gt; RXN02384

&lt;400&gt; 579

ctgatgagggc ggatatccgc aacatcgaca gcattgatga actccacact ttgccagctg 60

aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115  
Val Thr Arg Arg Leu  
1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163  
Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met  
10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211  
Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala  
25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259  
Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe  
40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307  
Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala  
55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355  
Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaaa atg				831
Trp Asn Met Gly Val Thr Gln	230	235		

&lt;210&gt; 580

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 580

Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn				
1	5	10	15	

Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu				
20	25	30		

Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn				
35	40	45		

Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala				
50	55	60		



Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg  
 65 70 75 80  
 Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu  
 85 90 95  
 Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro  
 100 105 110  
 Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg  
 115 120 125  
 Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp  
 130 135 140  
 Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu  
 145 150 155 160  
 Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser  
 165 170 175  
 Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr  
 180 185 190  
 Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala  
 195 200 205  
 Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln  
 210 215 220  
 Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln  
 225 230 235

&lt;210&gt; 581

&lt;211&gt; 453

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(430)

&lt;223&gt; RXN01560

&lt;400&gt; 581

atgggagcaa ggctcattta gctacttcga cgtggaagcg cacatcggtg agttgattcc 60

tgcacagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115  
 Val Gly Val Ser Tyr  
 1 5

atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163  
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys  
 10 15 20

att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211  
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly  
 25 30 35

acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259  
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

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          40              45              50
atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg 307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu
    55              60              65

ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca 355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
    70              75              80              85

ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac 403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
          90              95              100

ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc 450
Gly Val Asn Gly Pro Val Asp Ala Asn
          105              110

ttt 453

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<210> 582  
 <211> 110  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 582
Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
  1              5              10              15

Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
    20              25              30

Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
    35              40              45

Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
    50              55              60

His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
    65              70              75              80

Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
    85              90              95

Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
    100              105              110

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<210> 583  
 <211> 1137  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1114)  
 <223> RXN00667

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<400> 583
ggcatcagtg tttgaaggga aaagcagggtc aaacaagggtg cggtgattt gagcgatcac 60

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agcaccgaga tctgtgctga agaattcaat gattgggttg atg att gcg ttg aag 115
                                         Met Ile Ala Leu Lys
                                         1           5

tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta 163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu
                      10                      15                      20

ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac 211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp
                      25                      30                      35

gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg 259
Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr
                      40                      45                      50

cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt 307
Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg
                      55                      60                      65

ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc 355
Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro
    70                      75                      80                      85

gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc 403
Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro
                      90                      95                      100

gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac 451
Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp
                      105                      110                      115

gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct 499
Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro
                      120                      125                      130

cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg 547
Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu
    135                      140                      145

act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act 595
Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr
    150                      155                      160                      165

tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac 643
Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr
                      170                      175                      180

caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag gca atc 691
Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu Ala Ile
                      185                      190                      195

gca gaa ttc gtt cca ggg cta ctt gat gat ggt ccc gcg att tgg gaa 739
Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly Pro Ala Ile Trp Glu
    200                      205                      210

tcc cgc atc gaa aaa gaa cgc ggc atc gtg caa gcc ttc gtc gtg gaa 787
Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln Ala Phe Val Val Glu
    215                      220                      225

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ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835  
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu  
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883  
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg  
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931  
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu  
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979  
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu  
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg  
 1027  
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met  
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag  
 1075  
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu  
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt  
 1124  
 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu  
 330 335

agacatcacc cag  
 1137

<210> 584  
 <211> 338  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 584  
 Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys  
 1 5 10 15

Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val  
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu  
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu  
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly  
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp  
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His  
 100 105 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr  
 115 120 125  
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val  
 130 135 140  
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg  
 145 150 155 160  
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu  
 165 170 175  
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys  
 180 185 190  
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly  
 195 200 205  
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln  
 210 215 220  
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser  
 225 230 235 240  
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His  
 245 250 255  
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly  
 260 265 270  
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile  
 275 280 285  
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp  
 290 295 300  
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp  
 305 310 315 320  
 Pro Gln Thr Asn Glu Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly  
 325 330 335  
 Ser Leu

&lt;210&gt; 585

&lt;211&gt; 1281

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1258)

&lt;223&gt; RXC01711

&lt;400&gt; 585

tctcgtgagt ttctccccgg tagcaccttc tatatcagcc cccacgccgc gtcggagcag 60

gtgggatagc atcggcaacg cggttgcatg gccgttgcc atg ttg ttg atg gcg 115

												Met	Leu	Leu	Met	Ala	
												1				5	
cat	cgc	ttc	ttc	gtg	ctt	gcg	att	aac	ggc	gca	gtc	acc	gac	gat	ttc		163
His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe		
				10					15					20			
acg	acg	gtt	tat	agt	gct	tta	cga	cgt	ttc	gtt	gaa	ggt	att	ccg	gtc		211
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val		
			25					30					35				
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg		259
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro		
		40					45					50					
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg		307
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr		
		55				60					65						
ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	gtt	tta		355
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu		
70					75					80					85		
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggt	tgg	gcg	ctg	cgc	agc	atg		403
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met		
				90					95					100			
gtg	tgg	ccg	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa		451
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln		
			105					110					115				
aac	acc	ctc	att	ttc	tcc	aac	atc	aac	ggc	atc	ctg	ctg	ctc	atg	ttg		499
Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	Leu	Leu	Leu	Met	Leu		
		120					125					130					
gcg	att	ttc	ctg	tgg	tgc	gtg	gtg	cac	aaa	aaa	tcc	tgg	ttg	ggc	gga		547
Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	Ser	Trp	Leu	Gly	Gly		
	135					140					145						
cta	gtc	att	ggt	ttg	gcc	att	ttg	atc	aaa	ccc	atg	ttc	ctg	cca	ctt		595
Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	Met	Phe	Leu	Pro	Leu		
150					155					160					165		
ctc	ttc	cta	cct	ttg	gtg	aaa	aag	caa	tgg	gga	tcg	ctc	atc	ctc	ggc		643
Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly	Ser	Leu	Ile	Leu	Gly		
				170					175					180			
att	tta	acc	cca	gtg	att	ttc	aat	gca	gtg	gcc	tgg	ttc	tta	gtt	ccg		691
Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala	Trp	Phe	Leu	Val	Pro		
			185					190					195				
gga	gca	tct	gaa	tac	gtc	acc	cgc	acg	atg	ccc	tac	ctt	ggt	gaa	act		739
Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro	Tyr	Leu	Gly	Glu	Thr		
		200					205					210					
cga	gat	ttt	gcc	aac	agc	tca	ctc	cca	ggc	ttg	gcc	atc	tat	ttc	gga		787
Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Phe	Gly		
	215					220					225						
atg	ccc	acc	tgg	atg	gaa	atc	acc	tgg	ttc	ctc	atc	ttc	ggc	gca	atg		835
Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu	Ile	Phe	Gly	Ala	Met		

230							235							240							245	
gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca																	883					
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro																						
	250						255						260									
tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc																	931					
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe																						
	265						270						275									
ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct																	979					
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro																						
	280						285						290									
atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt																						
1027 Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val																						
	295						300						305									
gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc																						
1075 Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser																						
310	315						320						325									
cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc																						
1123 Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr																						
	330						335						340									
gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc																						
1171 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile																						
	345						350						355									
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att																						
1219 Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile																						
	360						365						370									
acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt																						
1268 Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala																						
	375						380						385									
caaactcatc agc																						
1281																						
<210> 586																						
<211> 386																						
<212> PRT																						
<213> Corynebacterium glutamicum																						
<400> 586																						
Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala																						
1 5 10 15																						
Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val																						
20 25 30																						
Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His																						

35					40					45						
Tyr	Leu	Tyr	Asn	Pro	Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	
50					55					60						
Ile	Thr	His	Phe	Thr	Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	
65					70					75					80	
Leu	Ala	Ile	Val	Leu	Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	
					85					90					95	
Ala	Leu	Arg	Ser	Met	Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	
					100					105					110	
Thr	Glu	Thr	Val	Gln	Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	
					115					120					125	
Leu	Leu	Leu	Met	Leu	Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	
130					135					140						
Ser	Trp	Leu	Gly	Gly	Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	
145					150					155					160	
Met	Phe	Leu	Pro	Leu	Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly	
					165					170					175	
Ser	Leu	Ile	Leu	Gly	Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala	
					180					185					190	
Trp	Phe	Leu	Val	Pro	Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro	
					195					200					205	
Tyr	Leu	Gly	Glu	Thr	Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu	
210					215					220						
Ala	Ile	Tyr	Phe	Gly	Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu	
225					230					235					240	
Ile	Phe	Gly	Ala	Met	Val	Gly	Leu	Ala	Val	Leu	Ala	Leu	Leu	Arg	Phe	
					245					250					255	
Arg	Asn	Thr	Glu	Pro	Tyr	Phe	Trp	Ala	Ala	Thr	Thr	Thr	Gly	Val	Leu	
					260					265					270	
Leu	Thr	Gly	Val	Phe	Phe	Leu	Ser	Ser	Leu	Gly	Gln	Met	Tyr	Tyr	Ser	
					275					280					285	
Met	Met	Ile	Phe	Pro	Met	Ile	Phe	Thr	Leu	Leu	Gly	Ser	Arg	Ser	Val	
290					295					300						
Phe	His	Asn	Trp	Val	Ala	Trp	Val	Ala	Ala	Tyr	Phe	Leu	Leu	Ser	Pro	
305					310					315					320	
Asp	Thr	Phe	Thr	Ser	Gln	Arg	Leu	Pro	Asp	Val	Ala	Arg	Trp	Met	Glu	
					325					330					335	
Phe	Phe	Ser	Ala	Thr	Val	Gly	Trp	Gly	Leu	Leu	Ile	Val	Val	Thr	Phe	
					340					345					350	
Val	Ser	Ala	Leu	Ile	Trp	Phe	Ile	Gly	Asp	Ile	Arg	Ala	Lys	Gly	Thr	
355					360					365						



Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg  
 370 375 380

Thr Ala  
 385

<210> 587

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> RXC02380

<400> 587

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tgctcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg 115  
 Met Thr Thr Thr Val  
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163  
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile  
 10 15 20

cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211  
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp  
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259  
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala  
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307  
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile  
 55 60 65

gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355  
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp  
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403  
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys  
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451  
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu  
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499  
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 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile  
 135 140 145

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 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala  
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 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg  
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 cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691  
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
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 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys  
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 Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
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 Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
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 Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
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 Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

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	Met Thr Thr Thr Val		
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Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile			
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His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp			
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Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala			
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Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile			
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Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp			
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Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys			
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His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile			
135 140 145			

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Met Ala Ile Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
170                      175                      180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
185                      190                      195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
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Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
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Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65          70          75          80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85          90          95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
100          105          110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
115          120          125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
130          135          140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
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Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
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Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val  
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 Val Ser Ala Leu Glu  
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 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys  
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 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile  
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 Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly  
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 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp  
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 Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe  
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 Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu  
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 Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp  
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 Val Leu Gly Ala Val  
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Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu	
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Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met	
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Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly	
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Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys	
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Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val	
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Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
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Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
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Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
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Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
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Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
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Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
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Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu  
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 Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val  
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 1939  
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
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 1987  
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2131
Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
665 670 675

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2179
Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
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Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
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745 750 755

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760 765 770

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825 830 835

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855 860 865

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2899

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920 925 930

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2947

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935 940 945

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2995

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950 955 960 965

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3043

Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
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Val Gly Trp

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<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

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Ile	Phe	Phe	Tyr	Gly	Leu	Phe	Ala	Leu	Phe	Met	Ala	Val	Leu	Asn	Thr
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Arg	Glu	Val	Phe	Lys	Pro	Gly	Ala	Trp	Ala	Pro	Val	Val	Asn	Asn	Val
			100					105					110		
Ile	Thr	Leu	Thr	Val	Leu	Gly	Val	Tyr	Met	Val	Leu	Pro	Ala	Arg	Leu
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His	Pro	His	Glu	Gln	Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu
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Gly	Val	Gly	Thr	Thr	Leu	Gly	Val	Val	Ala	Gln	Cys	Leu	Ile	Met	Ile
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Pro	Tyr	Leu	Arg	Arg	Ala	Gly	Ile	Asp	Met	Arg	Pro	Leu	Trp	Gly	Ile
				165					170					175	
Asp	Ala	Arg	Leu	Lys	Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val
			180					185					190		
Tyr	Val	Ala	Ile	Ser	Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala
	195						200					205			
Ser	Ile	Ala	Asp	Asp	Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met
	210					215					220				
Leu	Leu	Gln	Val	Pro	Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala
	225					230					235				240
Ile	Met	Pro	Arg	Leu	Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala
				245					250					255	
Val	Val	Ser	Asp	Leu	Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu
			260					265					270		
Ile	Pro	Ile	Val	Val	Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn
	275						280					285			
Gly	Leu	Phe	Ala	Tyr	Gly	Gln	Phe	Asp	Ala	Asn	Ala	Ala	Asn	Ile	Leu
	290					295					300				
Gly	Trp	Thr	Leu	Ser	Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu
	305					310					315				320
Val	Leu	Leu	His	Leu	Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr
				325					330					335	
Pro	Thr	Phe	Ile	Ile	Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser
			340					345					350		

Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
 435 440 445  
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480  
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
 485 490 495  
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
 500 505 510  
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
 515 520 525  
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
 530 535 540  
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
 610 615 620  
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
 660 665 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
 675 680 685  
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu  
 705 710 715 720  
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala  
 725 730 735  
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
 740 745 750  
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu  
 755 760 765  
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
 770 775 780  
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val  
 785 790 795 800  
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser  
 805 810 815  
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser  
 820 825 830  
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln  
 835 840 845  
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr  
 850 855 860  
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu  
 865 870 875 880  
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr  
 885 890 895  
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr  
 900 905 910  
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile  
 915 920 925  
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp  
 930 935 940  
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp  
 945 950 955 960  
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile  
 965 970 975  
 Ala Glu Val Gln Leu Val Gly Trp  
 980

&lt;210&gt; 595

&lt;211&gt; 915

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(892)

&lt;223&gt; RXA01807

&lt;400&gt; 595

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gcagtggctg gaactcggcg aggaaatcga gggctagtctc atg ccg tcg gca ggc 115  
 Met Pro Ser Ala Gly  
 1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163  
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg  
 10 15 20

gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggc 211  
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
 25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259  
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val  
 40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307  
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser  
 55 60 65

cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac 355  
 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp  
 70 75 80 85

ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc 403  
 Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly  
 90 95 100

tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag 451  
 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln  
 105 110 115

aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499  
 Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile  
 120 125 130

atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc 547  
 Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr  
 135 140 145

gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat 595  
 Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn  
 150 155 160 165

gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643  
 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu  
 170 175 180

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ctc ggc ccg ttt ggc gag tgg atc atc acc agc gcc act gaa act 691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Thr Ser Ala Thr Glu Thr
      185              190              195

gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu
      200              205              210

atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val
      215              220              225

tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile
      230              235              240              245

gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr
      250              255              260

aaa gcg ctt taggtttcgt ccgtctctga cag 915
Lys Ala Leu

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&lt;210&gt; 596

&lt;211&gt; 264

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 596

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Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
 1              5              10              15

Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
      20              25              30

Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
      35              40              45

Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
      50              55              60

Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
      65              70              75              80

Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
      85              90              95

Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
      100              105              110

Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
      115              120              125

Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
      130              135              140

Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
      145              150              155              160

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[illegible]

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<211> 1461
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1438)  
<223> RXN02754
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agttcactgt agctcccgct gattccgtag aatcaacaga																gtg	aat	acc	aat	ccg		115
																Val	Asn	Thr	Asn	Pro		
																1				5		
tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat																163						
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr																						
																10				20		
gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc																211						
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg																						
																25				35		
ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga																259						
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg																						
																40				50		
tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac																307						
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp																						
																55				65		
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac																355						
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp																						
																70				80		85
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat																403						
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp																						

90										95										100										
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451																													
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr																														
105 110 115																														
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499																													
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu																														
120 125 130																														
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547																													
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met																														
135 140 145																														
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595																													
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg																														
150 155 160 165																														
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643																													
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala																														
170 175 180																														
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691																													
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile																														
185 190 195																														
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739																													
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn																														
200 205 210																														
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787																													
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu																														
215 220 225																														
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835																													
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr																														
230 235 240 245																														
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883																													
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly																														
250 255 260																														
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931																													
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg																														
265 270 275																														
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc	979																													
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser																														
280 285 290																														
tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt																														
1027																														
Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val																														
295 300 305																														
gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca																														
1075																														
Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro																														
310 315 320 325																														

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg  
1123

Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val  
330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct  
1171

Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala  
345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac  
1219

Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc  
1267

Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
1315

Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro  
390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta  
1363

Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act  
1411

Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr  
425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca  
1458

Arg Phe Val Gly Phe Pro Pro Ala Ala  
440 445

aac  
1461

<210> 598

<211> 446

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 598

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Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp  
20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu  
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu  
 65 70 75 80  
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe  
 85 90 95  
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln  
 100 105 110  
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125  
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160  
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175  
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220  
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240  
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255  
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu  
 260 265 270  
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr  
 275 280 285  
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu  
 290 295 300  
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr  
 305 310 315 320  
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val  
 325 330 335  
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly  
 340 345 350  
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile  
 355 360 365  
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys  
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile  
385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys  
405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu  
420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala  
435 440 445

<210> 599

<211> 871

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> FRXA02405

<400> 599

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Val Asn Thr Asn Pro  
1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163  
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211  
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg  
25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259  
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg  
40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307  
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp  
55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355  
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp  
70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403  
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp  
90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451  
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr  
105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499  
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu  
120 125 130

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tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg 547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met
135 140 145

gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc 595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg
150 155 160 165

acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct 643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala
170 175 180

gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att 691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile
185 190 195

cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac 739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn
200 205 210

gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa 787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu
215 220 225

tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc 835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr
230 235 240 245

caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca 871
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro
250 255

<210> 600
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 600
Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
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20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
65 70 75 80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
85 90 95

Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
100 105 110

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Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
           115                          120                          125  
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
           130                          135                          140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
   145                          150                          155                          160  
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
                           165                          170                          175  
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
                           180                          185                          190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
           195                          200                          205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
   210                          215                          220  
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
   225                          230                          235                          240  
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
                           245                          250                          255  
 Pro

<210> 601  
 <211> 509  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(486)  
 <223> FRXA02754

<400> 601  
 ccc aca aac acc aag att gtg gtc tcc tcc gac ctg gat gaa ttc gcc 48  
 Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala  
   1                          5                          10                          15  
 atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96  
 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr  
           20                          25                          30  
 tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144  
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys  
           35                          40                          45  
 atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192  
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys  
   50                          55                          60  
 gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240  
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser  
   65                          70                          75                          80

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ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85                      90                      95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100                    105                    110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115                    120                    125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130                    135                    140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480
Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
      145                    150                    155                    160

gcc gct tagacaattc ggtctcacca aac 509
Ala Ala

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<210> 602  
 <211> 162  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 602
Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
  1                      5                      10                      15

Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
      20                    25                    30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
      35                    40                    45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
      50                    55                    60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
      65                    70                    75                    80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85                      90                      95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100                    105                    110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115                    120                    125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130                    135                    140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
      145                    150                    155                    160

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Ala Ala

&lt;210&gt; 603

&lt;211&gt; 960

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(937)

&lt;223&gt; RXA02112

&lt;400&gt; 603

tgaatccgtg gcggcaccgg cgcgagtcgc tttggaaagg atgctatctg ttgttccagc 60

agctcctggtt	actcctagct	cctcgaagga	tgcgtaattt	atg	act	acc	cat	att	115
				Met	Thr	Thr	His	Ile	
				1				5	

gac	cgc	atc	ggt	ggc	gca	gcg	tta	tcc	gag	gat	gcg	cca	tgg	ggc	gac	163
Asp	Arg	Ile	Val	Gly	Ala	Ala	Leu	Ser	Glu	Asp	Ala	Pro	Trp	Gly	Asp	
			10					15						20		

att	acc	tcc	gac	act	ttt	atc	cca	gga	tcg	gcg	cag	ctg	agc	gcc	aag	211
Ile	Thr	Ser	Asp	Thr	Phe	Ile	Pro	Gly	Ser	Ala	Gln	Leu	Ser	Ala	Lys	
			25					30					35			

ggt	ggt	gcc	cgg	gag	cca	ggt	gtg	ttc	agc	ggg	cag	gcg	ctt	tta	gac	259
Val	Val	Ala	Arg	Glu	Pro	Gly	Val	Phe	Ser	Gly	Gln	Ala	Leu	Leu	Asp	
		40				45						50				

gcc	tcc	ttc	cgg	ctc	gtc	gat	cct	agg	ata	aac	gca	tcc	ctt	aag	gtg	307
Ala	Ser	Phe	Arg	Leu	Val	Asp	Pro	Arg	Ile	Asn	Ala	Ser	Leu	Lys	Val	
	55					60					65					

gct	gat	ggt	gac	agc	ttt	gaa	acc	ggg	gac	atc	cta	gga	aca	att	acc	355
Ala	Asp	Gly	Asp	Ser	Phe	Glu	Thr	Gly	Asp	Ile	Leu	Gly	Thr	Ile	Thr	
70					75				80					85		

ggc	agt	gct	aga	agc	atc	ctc	cgt	tca	gag	cgc	att	gct	ctc	aac	ttc	403
Gly	Ser	Ala	Arg	Ser	Ile	Leu	Arg	Ser	Glu	Arg	Ile	Ala	Leu	Asn	Phe	
			90					95					100			

att	cag	agg	acg	tcc	ggc	atc	gct	aca	ttg	aca	tcg	tgc	tat	ggt	gca	451
Ile	Gln	Arg	Thr	Ser	Gly	Ile	Ala	Thr	Leu	Thr	Ser	Cys	Tyr	Val	Ala	
			105				110						115			

gag	ggt	aaa	ggc	acc	aaa	gcc	cgc	att	ggt	gat	acc	cgg	aaa	acc	aca	499
Glu	Val	Lys	Gly	Thr	Lys	Ala	Arg	Ile	Val	Asp	Thr	Arg	Lys	Thr	Thr	
		120				125					130					

ccc	ggc	ctg	cgc	atc	att	gaa	cgc	caa	gct	gtc	cgt	gac	ggg	ggc	gga	547
Pro	Gly	Leu	Arg	Ile	Ile	Glu	Arg	Gln	Ala	Val	Arg	Asp	Gly	Gly	Gly	
	135					140					145					

ttt	aat	cac	cga	gcc	acc	ttg	tcc	gat	gct	gtc	atg	gtg	aaa	gat	aac	595
Phe	Asn	His	Arg	Ala	Thr	Leu	Ser	Asp	Ala	Val	Met	Val	Lys	Asp	Asn	
150					155					160					165	

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cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg   643
His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu
      170                      175                      180

tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa   691
Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
      185                      190                      195

gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac   739
Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
      200                      205                      210

acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt   787
Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
      215                      220                      225

gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac   835
Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
      230                      235                      240                      245

ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc   883
Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
      250                      255                      260

gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat   931
Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp
      265                      270                      275

att ttc taatgctcta ccttgataat gca   960
Ile Phe

```

&lt;210&gt; 604

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 604

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Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp
  1                      5                      10                      15

Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala
      20                      25                      30

Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
      35                      40                      45

Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
      50                      55                      60

Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
      65                      70                      75                      80

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
      85                      90                      95

Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
      100                      105                      110

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Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp  
 115 120 125  
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val  
 130 135 140  
 Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val  
 145 150 155 160  
 Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser  
 165 170 175  
 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr  
 180 185 190  
 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu  
 195 200 205  
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln  
 210 215 220  
 Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala  
 225 230 235 240  
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly  
 245 250 255  
 Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu  
 260 265 270  
 Asp Leu Gly Leu Asp Ile Phe  
 275

&lt;210&gt; 605

&lt;211&gt; 1407

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1384)

&lt;223&gt; RXA02111

&lt;400&gt; 605

gcttgcgggga acaccgcacc gccaccccaa actgttcaga ttccaaagat aaattctgac 60

gctcattcca gccaccgtt tagaagaaaa gaccccaatc atg acc acc tca atc 115  
 Met Thr Thr Ser Ile  
 1 5

acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163  
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser  
 10 15 20

gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211  
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp  
 25 30 35

gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259  
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

40	45	50	
ccg cgc cag cag gtt ctc	ccc gag gag tac cag cgc gca agt gat gac		307
Pro Arg Gln Gln Val Leu	Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp		
55	60	65	
gaa ctg cat cgt agg atc	cgg gaa gcg aaa gac acc ctg ggt gac aaa		355
Glu Leu His Arg Arg Ile	Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys		
70	75	80	85
gtg gtt atc cta gga cac	ttc tac cag cgc gat gaa gtt atc caa cac		403
Val Val Ile Leu Gly His	Phe Tyr Gln Arg Asp Glu Val Ile Gln His		
90	95	100	
gca gat ttt gtt ggt gac	tct ttc caa ctt gcc cgc gct gcc aaa acc		451
Ala Asp Phe Val Gly Asp	Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr		
105	110	115	
cga ccc gag gcg gaa gcg	att gtg ttc tgc ggt gtg cac ttc atg gct		499
Arg Pro Glu Ala Glu Ala	Ile Val Phe Cys Gly Val His Phe Met Ala		
120	125	130	
gaa acc gct gat ctg tta	tcc acg gat gaa caa tca gtg atc ctc ccc		547
Glu Thr Ala Asp Leu Leu	Ser Thr Asp Glu Gln Ser Val Ile Leu Pro		
135	140	145	
aac ctt gcc gca ggt tgc	tcc atg gca gac atg gct gac ctt gat tcc		595
Asn Leu Ala Ala Gly Cys	Ser Met Ala Asp Met Ala Asp Leu Asp Ser		
150	155	160	165
gtc gaa gac tgc tgg gag	caa ctc acc tca att tat ggc gat gac acc		643
Val Glu Asp Cys Trp Glu	Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr		
170	175	180	
ctg atc cct gtg acc tac	atg aat tcc tct gca gcg ctc aaa ggt ttc		691
Leu Ile Pro Val Thr Tyr	Met Asn Ser Ser Ala Ala Leu Lys Gly Phe		
185	190	195	
gtg ggt gag cac ggc gga	att gta tgc acc tcc tca aat gca cgt tcc		739
Val Gly Glu His Gly Gly	Ile Val Cys Thr Ser Ser Asn Ala Arg Ser		
200	205	210	
gta ttg gag tgg gcg ttt	gaa cgc ggc caa cga gtc ctg ttc ttc ccc		787
Val Leu Glu Trp Ala Phe	Glu Arg Gly Gln Arg Val Leu Phe Phe Pro		
215	220	225	
gat cag cac ttg ggt cga	aac acc gcg aaa gcc atg ggc att ggg atc		835
Asp Gln His Leu Gly Arg	Asn Thr Ala Lys Ala Met Gly Ile Gly Ile		
230	235	240	245
gat caa atg ccc ctg tgg	aat ccc aac aaa cca ctg ggt ggc aac acc		883
Asp Gln Met Pro Leu Trp	Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr		
250	255	260	
gtt tcc gag cta gaa aac	gca aag gta ctg ctc tgg cat ggt ttc tgc		931
Val Ser Glu Leu Glu Asn	Ala Lys Val Leu Leu Trp His Gly Phe Cys		
265	270	275	
tct gta cac aag cgc ttt	act gtc gag cag atc aac aaa gcc cgc gcc		979
Ser Val His Lys Arg Phe	Thr Val Glu Gln Ile Asn Lys Ala Arg Ala		
280	285	290	

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca  
1027

Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro  
295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa  
1075

Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys  
310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa  
1123

Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu  
330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc  
1171

Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile  
345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att  
1219

Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile  
360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac  
1267

His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn  
375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga  
1315

Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg  
390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act  
1363

Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr  
410 415 420

cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga  
1407

Pro Ser Ser Ser Lys Asp Ala  
425

<210> 606

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala  
1 5 10 15

Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln  
20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro  
35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln  
 50 55 60  
 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp  
 65 70 75 80  
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp  
 85 90 95  
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala  
 100 105 110  
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly  
 115 120 125  
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln  
 130 135 140  
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met  
 145 150 155 160  
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile  
 165 170 175  
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala  
 180 185 190  
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser  
 195 200 205  
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg  
 210 215 220  
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala  
 225 230 235 240  
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro  
 245 250 255  
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu  
 260 265 270  
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile  
 275 280 285  
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro  
 290 295 300  
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr  
 305 310 315 320  
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe  
 325 330 335  
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr  
 340 345 350  
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser  
 355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu  
 370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val  
 385 390 395 400

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro  
 405 410 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala  
 420 425

&lt;210&gt; 607

&lt;211&gt; 954

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(931)

&lt;223&gt; RXA01073

&lt;400&gt; 607

taaccgactc cagcactaaa ctccaaaccc ttggcccgca ccgccaaagt ttagcgcgcc 60

ccaagacacc accgcgccat gtttgcctag gattaggtac atg aca aac act caa 115  
 Met Thr Asn Thr Gln  
 1 5

acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163  
 Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala  
 10 15 20

aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211  
 Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala  
 25 30 35

tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259  
 Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser  
 40 45 50

act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307  
 Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala  
 55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355  
 Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr  
 70 75 80 85

gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403  
 Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile  
 90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451  
 Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala  
 105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499  
 Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp  
 120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547  
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr  
 135 140 145  
  
 gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595  
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala  
 150 155 160 165  
  
 gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643  
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala  
 170 175 180  
  
 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691  
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile  
 185 190 195  
  
 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739  
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr  
 200 205 210  
  
 gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787  
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu  
 215 220 225  
  
 ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835  
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp  
 230 235 240 245  
  
 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883  
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly  
 250 255 260  
  
 cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931  
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg  
 265 270 275  
  
 taatccaaca gtttgagtgt cgc 954

&lt;210&gt; 608

&lt;211&gt; 277

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 608

Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro  
 1 5 10 15  
  
 Ala Ile Asp Val Ala Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val  
 20 25 30  
  
 Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser  
 35 40 45  
  
 Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val  
 50 55 60  
  
 Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala  
 65 70 75 80



867

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc	211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg	
25 30 35	
ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga	259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg	
40 45 50	
tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac	307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp	
55 60 65	
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac	355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp	
70 75 80 85	
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat	403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp	
90 95 100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	
105 110 115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	
120 125 130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	
250 255 260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg  
 265 270 275  
 aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979  
 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser  
 280 285 290  
 tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt  
 1027  
 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val  
 295 300 305  
 gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca  
 1075  
 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro  
 310 315 320 325  
 acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg  
 1123  
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val  
 330 335 340  
 gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct  
 1171  
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala  
 345 350 355  
 gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac  
 1219  
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
 360 365 370  
 cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc  
 1267  
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
 375 380 385  
 ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
 1315  
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro  
 390 395 400 405  
 act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta  
 1363  
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
 410 415 420  
 cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act  
 1411  
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr  
 425 430 435  
 cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca  
 1458  
 Arg Phe Val Gly Phe Pro Pro Ala Ala  
 440 445  
 aac  
 1461

&lt;210&gt; 610

&lt;211&gt; 446

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 610

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu  
 1 5 10 15

Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp  
 20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu  
 35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
 50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu  
 65 70 75 80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe  
 85 90 95

Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln  
 100 105 110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255

Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu  
 260 265 270

Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr  
 275 280 285

Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu

290					295					300					
Arg 305	Gly	Glu	Pro	Val	Asp 310	Val	Phe	Gly	Val	Gly 315	Thr	Ser	Val	Val	Thr 320
Gly	Ser	Gly	Ala	Pro 325	Thr	Ala	Gly	Leu	Val 330	Tyr	Lys	Ile	Gly	Glu	Val 335
Ala	Gly	His	Pro 340	Val	Ala	Lys	Arg	Ser 345	Arg	Asn	Lys	Glu	Ser	Tyr	Gly
Gly	Gly	Lys 355	Lys	Ala	Val	Arg	Thr 360	His	Arg	Lys	Ser	Gly 365	Thr	Ala	Ile
Glu	Glu 370	Ile	Val	Tyr	Pro	Phe 375	Asn	Ala	Glu	Ala	Pro 380	Asp	Thr	Gly	Lys
Leu 385	Asp	Thr	Leu	Ser	Leu 390	Thr	Ile	Pro	Leu	Met 395	Arg	Asp	Gly	Glu	Ile 400
Val	Pro	Gly	Leu	Pro 405	Thr	Leu	Glu	Asp	Ser 410	Arg	Ala	Tyr	Leu	Ala	Lys
Gln	Leu	Val	Ser 420	Leu	Pro	Trp	Glu	Gly 425	Leu	Ala	Leu	Ser	Arg	Asp	Glu
Pro	Val	Leu 435	His	Thr	Arg	Phe	Val 440	Gly	Phe	Pro	Pro	Ala	Ala		

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<210> 611
<211> 531
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (508)  
<223> RXA02299
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<400> 611  
acgcgggggt tgttgccgga tcgaaatatt cctttccttg tcatctcacg ctatgatttc 60

taaaacttgc aggacaacc ccataaggac accacaggac atg ctg cgc acc atc 115  
Met Leu Arg Thr Ile  
1 5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163  
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp  
10 15 20

tat	ggt	ggc	tct	gta	acc	atc	gac	gcc	gac	ctg	ggt	cac	gcc	gcc	gga	211
Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu	Val	His	Ala	Ala	Gly	
			25					30					35			

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259  
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala  
40 45 50

cg t ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307  
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile

55	60	65	
tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg			355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val			
70	75	80	85
atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat			403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr			
	90	95	100
gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc			451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu			
	105	110	115
ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg			499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser			
	120	125	130
aga agc att tagcggtttta gctcgccaat att			531
Arg Ser Ile			
135			

&lt;210&gt; 612

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 612

Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr			
1	5	10	15
Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu			
	20	25	30
Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp			
	35	40	45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala			
	50	55	60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn			
	65	70	75
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala			
	85	90	95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn			
	100	105	110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser			
	115	120	125
Gly Leu Leu Thr Ser Arg Ser Ile			
	130	135	

&lt;210&gt; 613

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(937)

&lt;223&gt; RXA01928

&lt;400&gt; 613

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gcgagtagcgc caccttgggc gattccttgc acgacgccgc gcaggcctac atcgccgata 60

tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
                                     Met Gln Val Ala Thr
                                     1 5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
                                     10 15 20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211
Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
                                     25 30 35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259
Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
                                     40 45 50

aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307
Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
                                     55 60 65

tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355
Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
                                     70 75 80 85

gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403
Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly
                                     90 95 100

ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451
Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
                                     105 110 115

ggg gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499
Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
                                     120 125 130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547
Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
                                     135 140 145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595
Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
                                     150 155 160 165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643
Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
                                     170 175 180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691
Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
                                     185 190 195

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caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739
Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys
      200                      205                      210

gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787
Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala
      215                      220                      225

agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835
Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala
      230                      235                      240                      245

acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883
Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu
      250                      255                      260

gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931
Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile
      265                      270                      275

gag ctc tagtaccac cctgcgttgc agc 960
Glu Leu

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<210> 614  
 <211> 279  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

```

<400> 614
Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His
 1                      5                      10                      15

His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly
      20                      25                      30

His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val
      35                      40                      45

Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys
      50                      55                      60

Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu
      65                      70                      75                      80

Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu
      85                      90                      95

Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile
      100                      105                      110

Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val
      115                      120                      125

Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala
      130                      135                      140

Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu
      145                      150                      155                      160

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Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile  
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser  
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly  
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala  
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu  
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu  
 245 250 255

Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg  
 260 265 270

Leu Ile Asp Asn Ile Glu Leu  
 275

&lt;210&gt; 615

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(913)

&lt;223&gt; RXN01929

&lt;400&gt; 615

aaaatttgac tccataacga gaacttaatc gagcaacacc cctgaacagt gaatcaaadc 60

ggaatttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115  
 Met Pro Met Ser Gly  
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163  
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val  
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211  
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala  
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259  
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser  
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307  
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu  
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355  
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg  
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403  
Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro  
90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451  
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala  
105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499  
Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg  
120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547  
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr  
135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595  
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly  
150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643  
Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala  
170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691  
Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg  
185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739  
Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly  
200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787  
Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu  
215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835  
Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly  
230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883  
Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala  
250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933  
Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
265 270

aag 936

&lt;210&gt; 616

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 616

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe  
1 5 10 15

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr  
                   20                  25                  30  
 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu  
                   35                  40                  45  
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr  
                   50                  55                  60  
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
                   65                  70                  75                  80  
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
                   85                  90                  95  
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
                   100                  105                  110  
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
                   115                  120                  125  
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly  
                   130                  135                  140  
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val  
                   145                  150                  155                  160  
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg  
                   165                  170                  175  
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro  
                   180                  185                  190  
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile  
                   195                  200                  205  
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln  
                   210                  215                  220  
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu  
                   225                  230                  235                  240  
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile  
                   245                  250                  255  
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
                   260                  265                  270

&lt;210&gt; 617

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; FRXA01929

&lt;400&gt; 617

tgactccata acgagaactt aatcgagcaa cacccttgaa cagtgaatca aatcggaatt 60

tattttattct	gagctgggtca	tcacatcttat	actcatgccc	atg	tca	ggc	att	gat	115
				Met	Ser	Gly	Ile	Asp	
				1				5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163								
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly									
	10 15 20								
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211								
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile									
	25 30 35								
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259								
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala									
	40 45 50								
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307								
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu									
	55 60 65								
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355								
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu									
	70 75 80 85								
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403								
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln									
	90 95 100								
gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg	451								
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala									
	105 110 115								
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499								
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile									
	120 125 130								
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547								
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln									
	135 140 145								
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595								
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser									
	150 155 160 165								
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643								
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala									
	170 175 180								
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691								
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val									
	185 190 195								
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739								
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly									
	200 205 210								
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787								
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg									
	215 220 225								

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835  
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser  
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883  
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr  
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930  
 Phe Pro Gly Glu Ala Glu Ser Phe  
 265

<210> 618

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu  
 1 5 10 15

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala  
 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
 225 230 235 240  
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
 245 250 255  
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 260 265

<210> 619  
 <211> 921  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(898)  
 <223> RXA01521

<400> 619  
 accccggcag gcaacgcctt ttccgggatt tggcgcgcag gcaggcagag atttcccgcg 60  
 cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115  
 Leu Ser Phe Thr His  
 1 5  
 ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163  
 Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly  
 10 15 20  
 agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211  
 Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly  
 25 30 35  
 aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259  
 Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg  
 40 45 50  
 atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307  
 Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp  
 55 60 65  
 cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355  
 His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn  
 70 75 80 85  
 ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403  
 Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly  
 90 95 100  
 cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451  
 Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu  
 105 110 115  
 ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499  
 Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr  
 120 125 130  
 gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547  
 Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc			595
Val Lys Leu His Ser	Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala		
150	155	160	165
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca			643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala			
	170	175	180
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac			691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His			
	185	190	195
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca			739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala			
	200	205	210
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca			787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro			
	215	220	225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc			835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly			
	230	235	240
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc			883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe			
	250	255	260
aaa aac atc gaa ggc tgatecccggt ttacccagtt cgc			921
Lys Asn Ile Glu Gly			
	265		

&lt;210&gt; 620

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln			
1	5	10	15
Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val			
	20	25	30
Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile			
	35	40	45
Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala			
	50	55	60
Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala			
	65	70	75
Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val			
	85	90	95
Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr			
	100	105	110

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu  
           115                                  120                                  125  
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn  
           130                                  135                                  140  
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met  
 145                                  150                                  155                                  160  
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp  
                                   165                                  170                                  175  
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala  
                                   180                                  185                                  190  
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln  
           195                                  200                                  205  
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly  
           210                                  215                                  220  
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala  
 225                                  230                                  235                                  240  
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro  
                                   245                                  250                                  255  
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly  
           260                                  265

<210> 621  
 <211> 1137  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1114)  
 <223> RXS01145

<400> 621  
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 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
   Met Ala Ile Glu Leu  
   1                                  5  
  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
                                   10                                  15                                  20  
  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
                                   25                                  30                                  35  
  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
           40                                  45                                  50



tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac  
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
330 335

ccctttgacg gct  
1137

<210> 622

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 622

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205  
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220  
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240  
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255  
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270  
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285  
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300  
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
 305 310 315 320  
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335  
 Thr Ala

<210> 623  
 <211> 556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(556)  
 <223> FRXA01145

<400> 623  
 taatgtagtt gtctgcccaa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60  
  
 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
 Met Ala Ile Glu Leu  
 1 5  
  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50  
  
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
135 140 145

tgc ctc atc 556  
Cys Leu Ile  
150

&lt;210&gt; 624

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 624

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile  
145 150

<210> 625  
<211> 1389  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1366)  
<223> RXA02239

<400> 625  
ctatgcacag cggaggtcga gggagagcgt ggggtggcgt cgaaaagcat cttgtagagt 60  
gtgtgggaac ccagccagcc tcttactttg aaggattggt gtg ccc atg act cat 115  
Val Pro Met Thr His  
1 5  
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163  
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly  
10 15 20  
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211  
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu  
25 30 35  
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259  
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe  
40 45 50  
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307  
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr  
55 60 65  
acg gtg ttt gat gcg gtg gat tcg gtg cag cat gtg aaa gtt ggc cag 355  
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln  
70 75 80 85  
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403  
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala  
90 95 100  
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451  
Arg Val Val Ala Gly Leu Gly Asp Asn Leu Leu Ala Ala Thr Leu Leu  
105 110 115  
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499  
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met  
120 125 130  
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547  
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg  
135 140 145  
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595  
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp  
150 155 160 165

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc 643  
 Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala  
 170 175 180

aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag 691  
 Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys  
 185 190 195

aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg 739  
 Lys Val Leu Ile Thr Ala Gly Thr His Glu His Ile Asp Pro Val  
 200 205 210

cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt 787  
 Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly  
 215 220 225

gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat 835  
 Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn  
 230 235 240 245

gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg 883  
 Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val  
 250 255 260

tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct 931  
 Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser  
 265 270 275

gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg 979  
 Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser  
 280 285 290

cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca  
 1027  
 Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala  
 295 300 305

ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg  
 1075  
 Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr  
 310 315 320 325

gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtg  
 1123  
 Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val  
 330 335 340

ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat  
 1171  
 Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr  
 345 350 355

gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat  
 1219  
 Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn  
 360 365 370

gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg  
 1267  
 Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp  
 375 380 385

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa  
1315

Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys  
390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa  
1363

Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu  
410 415 420

gtc tagaaaaatc cagctagacc act

1389

Val

<210> 626

<211> 422

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 626

Val Pro Met Thr His Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val  
1 5 10 15

Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val  
20 25 30

Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu  
35 40 45

Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly  
50 55 60

Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His  
65 70 75 80

Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr  
85 90 95

Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu  
100 105 110

Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala  
115 120 125

Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala  
130 135 140

Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg  
145 150 155 160

Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln  
165 170 175

Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln  
180 185 190

Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu  
195 200 205

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His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln
 210                               215                               220

Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser
225                               230                               235                               240

Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu
                               245                               250                               255

Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu
                               260                               265                               270

Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp
                               275                               280                               285

Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp
 290                               295                               300

Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp
305                               310                               315                               320

Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser
                               325                               330                               335

Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr
                               340                               345                               350

Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp
                               355                               360                               365

Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys
 370                               375                               380

His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val
385                               390                               395                               400

Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala
                               405                               410                               415

Leu Ala Tyr Arg Glu Val
                               420

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&lt;210&gt; 627

&lt;211&gt; 1092

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1069)

&lt;223&gt; RXA00581

&lt;400&gt; 627

gcatgagttt actcacgtgc ccacgtcttt tagccacca ttgaagttaa aaaataaccc 60

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cgatcacact agtggagtag ctaagggtgca caatggattc atg gca gag caa aac 115
                Met Ala Glu Gln Asn

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1

5



gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc	163
Ala Ala Ser Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe	
10 15 20	
agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac	211
Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn	
25 30 35	
tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc	259
Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly	
40 45 50	
atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg	307
Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro	
55 60 65	
ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act	355
Leu Ser Arg Leu Ile His Leu Gln Val Ala Arg Gln Gln Leu Thr	
70 75 80 85	
gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg	403
Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro	
90 95 100	
ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc	451
Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr	
105 110 115	
gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc	499
Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg	
120 125 130	
gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta	547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu	
135 140 145	
atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac	595
Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp	
150 155 160 165	
caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc	643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu	
170 175 180	
gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca	691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro	
185 190 195	
ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc	739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly	
200 205 210	
tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc	787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe	
215 220 225	
gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg	835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp	
230 235 240 245	
tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc	883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro  
 250 255 260  
 ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931  
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile  
 265 270 275  
 gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979  
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val  
 280 285 290  
 gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa  
 1027  
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys  
 295 300 305  
 ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc  
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 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile  
 310 315 320  
 taggggttct tgctggtttt gag  
 1092  
 <210> 628  
 <211> 323  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 628  
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 20 25 30  
 Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val  
 35 40 45  
 Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala  
 50 55 60  
 Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala  
 65 70 75 80  
 Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro  
 85 90 95  
 Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val  
 100 105 110  
 Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp  
 115 120 125  
 Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr  
 130 135 140  
 Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe  
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val  
 165 170 175

Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala  
 180 185 190

Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile  
 195 200 205

Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met  
 210 215 220

Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu  
 225 230 235 240

Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr  
 245 250 255

Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala  
 260 265 270

Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn  
 275 280 285

Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser  
 290 295 300

Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met  
 305 310 315 320

Arg Lys Ile

<210> 629  
 <211> 1023  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1000)  
 <223> RXS00838

<400> 629  
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tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115  
 Met Lys Ile Ala Ile  
 1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu  
 10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211  
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala  
 25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259  
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

40	45	50	
gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat			307
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp			
55	60	65	
gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct			355
Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala			
70	75	80	85
gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag			403
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln			
	90	95	100
aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat			451
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp			
	105	110	115
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca			499
Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro			
	120	125	130
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat			547
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp			
	135	140	145
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt			595
Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly			
150	155	160	165
att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa			643
Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys			
	170	175	180
gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag			691
Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys			
	185	190	195
caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg			739
Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu			
	200	205	210
atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg			787
Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro			
	215	220	225
agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag			835
Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu			
230	235	240	245
aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt			883
Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser			
	250	255	260
gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg			931
Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val			
	265	270	275
ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg			979
Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu			
	280	285	290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg

1023

Lys Glu Glu Glu Asn Ser Leu  
295 300

<210> 630

<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 630

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly  
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Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly  
20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala  
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg  
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val  
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys  
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe  
115 120 125

Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser  
130 135 140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr  
145 150 155 160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val  
165 170 175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly  
180 185 190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala  
195 200 205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala  
210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala  
225 230 235 240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala  
245 250 255

Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg  
260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr  
275 280 285

Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu  
290 295 300

<210> 631

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (385)

<223> RXC02238

<400> 631

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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115  
Val Thr Asn Val Ser  
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt      307  
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
          55                        60                               65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
90 95

**cac** 408

<210> 632

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp

1	5	10	15
Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys	20	25	30
Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg	35	40	45
Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe	50	55	60
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile	65	70	75
Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly	85	90	95

&lt;210&gt; 633

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(583)

&lt;223&gt; RXN03058

&lt;400&gt; 633

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acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaata tagagctcat 60
gccatttgg aatcacaaca ccgcataatcg gccatggctg gtg tca aag ctc aaa 115
                                     Val Ser Lys Leu Lys
                                     1 5
ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
10 15 20
gac ctg gcc ggc cgc cag gtc ggc cat gtc gat gtc gtg gat cct ctt 211
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
25 30 35
att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
40 45 50
atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
55 60 65
aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
70 75 80 85
ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
90 95 100
caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln

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          105          110          115
atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
          120          125          130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
          135          140          145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
          150          155          160

tataaaccaa aaa 606

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<210> 634  
 <211> 161  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 634
Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
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Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
          20              25              30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
          35              40              45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
          50              55              60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
          65              70              75              80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
          85              90              95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
          100              105              110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
          115              120              125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
          130              135              140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
          145              150              155              160

Pro

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<210> 635  
 <211> 606  
 <212> DNA  
 <213> *Corynebacterium glutamicum*



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(583)

&lt;223&gt; FRXA02903

&lt;400&gt; 635

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 Val Ser Lys Leu Lys  
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163  
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala  
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211  
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu  
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259  
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala  
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307  
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu  
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355  
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val  
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403  
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu  
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451  
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln  
 105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499  
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile  
 120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547  
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly  
 135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593  
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro  
 150 155 160

tataaaccaa aaa 606

&lt;210&gt; 636

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 636

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly  
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Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp  
 20 25 30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr  
 35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
 50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
 65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
 85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
 100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu  
 115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg  
 130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys  
 145 150 155 160

Pro

&lt;210&gt; 637

&lt;211&gt; 783

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(760)

&lt;223&gt; RXA00166

&lt;400&gt; 637

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gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115  
 Val Glu Leu Ala Arg  
 1 5

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163  
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
 10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211  
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp  
 25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

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Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln
      40              45              50

gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att 307
Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile
      55              60              65

acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg 355
Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala
      70              75              80              85

gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg 403
Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp
      90              95              100

aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att 451
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile
      105              110              115

atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca 499
Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala
      120              125              130

gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac 547
Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His
      135              140              145

ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg 595
Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp
      150              155              160              165

tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag 643
Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln
      170              175              180

tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa 691
Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu
      185              190              195

ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg 739
Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu
      200              205              210

gca ggc aga tct tcc aat ctt taggagccct cgccatgtac ctg 783
Ala Gly Arg Ser Ser Asn Leu
      215              220

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&lt;210&gt; 638

&lt;211&gt; 220

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 638

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Val Glu Leu Ala Arg Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly
  1              5              10              15

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Thr Gly Lys Leu Thr Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu
      20              25              30

```

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Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala

```

```

          35              40              45
Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn
  50              55              60
Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val
  65              70              75              80
Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala
          85              90              95
Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His
          100              105              110
Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe
          115              120              125
Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr
          130              135              140
Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His
          145              150              155              160
Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val
          165              170              175
Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro
          180              185              190
Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser
          195              200              205
Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu
          210              215              220

<210> 639
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> RXA00633

<400> 639
aaagctgctgga taattaaaaa cacttagcgc caaaaattga acactgttca attaacctat 60

tacactgcag atatacatcc aaaccaagtg acggaggaaa atg gaa aac ccc agc 115
Met Glu Asn Pro Ser
          1              5

ttg cgc gag ctt gat cac cga aac atc tgg cac ccg tat gcc gcg ccg 163
Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro
          10              15              20

ggc gtg cgc aat aga ctc gtc acc aaa acc gat gga gtg ttt ttg acg 211
Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp Gly Val Phe Leu Thr
          25              30              35

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ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tcg	259
Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser	
40 45 50	
gca att cat gga cac gga cac ccc cga ctg aaa gct gcc gcc caa aaa	307
Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Ala Gln Lys	
55 60 65	
caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag	355
Gln Ile Asp Thr Met Ser His Val Met Phe Gly Gly Leu Thr His Glu	
70 75 80 85	
ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc	403
Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser	
90 95 100	
ttt gac cac gtc ttt tat tcc gat tcg ggc tcg gtc tca gtg gag gtc	451
Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val	
105 110 115	
gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa	499
Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu	
120 125 130	
cgg aca aaa ctc ctc acc tgg cgg tcc ggc tac cac gga gac aca ttc	547
Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe	
135 140 145	
acc gcg atg agc gtg tgc gac cca gaa aat ggc atg cat agc ctc tgg	595
Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp	
150 155 160 165	
aaa ggc aca ctc ccc gag cag att ttc gcc ccc gcc cca cca gtt cgg	643
Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Pro Val Arg	
170 175 180	
ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg	691
Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu Arg Ser Met Glu Leu	
185 190 195	
ctt atc gac gag gcg gtc tcc gca atc atc atc gaa ccg atc gtc caa	739
Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile Glu Pro Ile Val Gln	
200 205 210	
ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc att gaa gga gtc	787
Gly Ala Gly Gly Met Arg Phe His Asp Val Ala Leu Ile Glu Gly Val	
215 220 225	
gcc aca ctg tgc aag aag cac gat cgt ttc ttg atc gtc gat gaa att	835
Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu Ile Val Asp Glu Ile	
230 235 240 245	
gcc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat	883
Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe Ala Thr Leu Ser Asn	
250 255 260	
ggc cta caa cca gac atc atg tgt gtg ggc aag gcc ctc acc ggt gga	931
Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly	
265 270 275	
ttc atg tcc ttc gcc gct act tta tgc acg gac aag gtg gct caa tta	979

Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu  
 280 285 290  
 atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt  
 1027  
 Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe  
 295 300 305  
 atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc  
 1075  
 Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile  
 310 315 320 325  
 att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa  
 1123  
 Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu  
 330 335 340  
 ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat  
 1171  
 Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp  
 345 350 355  
 gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc  
 1219  
 Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val  
 360 365 370  
 aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc  
 1267  
 Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile  
 375 380 385  
 cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg  
 1315  
 Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr  
 390 395 400 405  
 tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa  
 1363  
 Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys  
 410 415 420  
 ggg aaa taaaccatgc catttttatt tgt  
 1392  
 Gly Lys

&lt;210&gt; 640

&lt;211&gt; 423

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His  
 1 5 10 15

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp  
 20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met  
           35                          40                          45  
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys  
           50                          55                          60  
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly  
           65                          70                          75                          80  
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn  
                           85                          90                          95  
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser  
                           100                          105                          110  
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly  
           115                          120                          125  
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr  
           130                          135                          140  
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly  
           145                          150                          155                          160  
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro  
                           165                          170                          175  
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu  
                           180                          185                          190  
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile  
           195                          200                          205  
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala  
           210                          215                          220  
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu  
           225                          230                          235                          240  
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe  
                           245                          250                          255  
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys  
           260                          265                          270  
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp  
           275                          280                          285  
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met  
           290                          295                          300  
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His  
           305                          310                          315                          320  
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys  
                           325                          330                          335  
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu  
           340                          345                          350  
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

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355              360              365
Met Glu Gln Asn Val Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp
370              375              380

His Gly Val Trp Ile Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro
385              390              395              400

Pro Tyr Ile Thr Thr Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu
405              410              415

His Ala Ala Val Lys Gly Lys
420

<210> 641
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXA00632

<400> 641
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ctgcactgcg cttcatgctg cagttaaagg gaaataaacc atg cca ttt tta ttt 115
Met Pro Phe Leu Phe
1 5

gtc agc ggt acc gga act ggg gtt ggg aaa acc ttc tcc aca gcc gtt 163
Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr Phe Ser Thr Ala Val
10 15 20

ttg gtt cga tac tta gcc gat caa gga cac gat gtt ctg ccc gta aag 211
Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp Val Leu Pro Val Lys
25 30 35

cta gtc caa acc ggt gaa ctt cca ggc gag gga gac atc ttt aac att 259
Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly Asp Ile Phe Asn Ile
40 45 50

gaa cgc ttg act gga att gct gga gag gaa ttt gct cgt ttc aaa gac 307
Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe Ala Arg Phe Lys Asp
55 60 65

cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata 355
Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu Gly Val Glu Pro Ile
70 75 80 85

cag ttt gat cag att atc tcg tgg ctt cgt ggt ttt gac gac cca gat 403
Gln Phe Asp Gln Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp
90 95 100

cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg gtc aga tta ggg 451
Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly
105 110 115

gaa gat ttc acc ctg gca gat gtt gcc tcc gct ttg aat gca ccc tta 499

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Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu  
           120                                  125                                  130  
  
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547  
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu  
           135                                  140                                  145  
  
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595  
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu  
           150                                  155                                  160                                  165  
  
 ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643  
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu  
                                   170                                  175                                  180  
  
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691  
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro  
                                   185                                  190                                  195  
  
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739  
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro  
           200                                  205                                  210  
  
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792  
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg  
           215                                  220  
  
 tcg 795

&lt;210&gt; 642

&lt;211&gt; 224

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 642

Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr  
           1                                  5                                  10                                  15  
  
 Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp  
                                   20                                  25                                  30  
  
 Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly  
           35                                  40                                  45  
  
 Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe  
           50                                  55                                  60  
  
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu  
           65                                  70                                  75                                  80  
  
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly  
                                   85                                  90                                  95  
  
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu  
           100                                  105                                  110  
  
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala  
           115                                  120                                  125  
  
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

130	135	140
Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr		
145	150	155
Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala		
	165	170
Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe		
	180	185
Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu		
	195	200
Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg		
210	215	220

<210> 643  
 <211> 1125  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1102)  
 <223> RXA00295

<400> 643  
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 ttaagcgcgc agttattgac aaccagcctc taggagatcc atg acc atc ccc ggc 115  
 Met Thr Ile Pro Gly  
 1 5  
 acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163  
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly  
 10 15 20  
 ctt aat cag cag cag ttg atg gag gtt ctc acc ttg cct gaa gag caa 211  
 Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr Leu Pro Glu Glu Gln  
 25 30 35  
 atc cca gac ttg atg gaa tta gcc cac cag gtt cgg ttg aag tgg tgt 259  
 Ile Pro Asp Leu Met Glu Leu Ala His Gln Val Arg Leu Lys Trp Cys  
 40 45 50  
 ggg gaa gaa atc gag gtc gag gcc att att tcc ctc aaa act ggc ggt 307  
 Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser Leu Lys Thr Gly Gly  
 55 60 65  
 tgc cct gaa gat tgt cat ttc tgc tca cag tct ggg ttg ttt gaa tcg 355  
 Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser Gly Leu Phe Glu Ser  
 70 75 80 85  
 ccg gtg cgt tcg gtg tgg ctg gat att ccg aat ctg gtt gaa gcc gct 403  
 Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn Leu Val Glu Ala Ala  
 90 95 100

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aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca 451
Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala
105 110 115

gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc 499
Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Glu Ala Val
120 125 130

ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga 547
Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly
135 140 145

acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc gcc gtc cac 595
Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Ala Gly Val His
150 155 160 165

cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt 643
Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val
170 175 180

gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg 691
Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val
185 190 195

gca gaa gct gga atg gaa gtc tgt tcc gcc gga atc tta gga atg gcc 739
Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly
200 205 210

gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt 787
Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu
215 220 225

gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg gcc acc 835
Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr
230 235 240 245

cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct 883
Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser
250 255 260

att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct 931
Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala
265 270 275

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979
Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu
280 285 290

ctg gga gcc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc
1027
Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu
295 300 305

ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg
1075
Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu
310 315 320 325

ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcataaac
1122

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Pro Ile Lys Val Leu Asn Lys Val Ile  
330

gac  
1125

<210> 644  
<211> 334  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 644  
Met Thr Ile Pro Gly Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu  
1 5 10 15  
Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr  
20 25 30  
Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val  
35 40 45  
Arg Leu Lys Trp Cys Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser  
50 55 60  
Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser  
65 70 75 80  
Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn  
85 90 95  
Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe  
100 105 110  
Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln  
115 120 125  
Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val  
130 135 140  
Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala  
145 150 155 160  
Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser  
165 170 175  
Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu  
180 185 190  
Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly  
195 200 205  
Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val  
210 215 220  
Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp  
225 230 235 240  
Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg  
245 250 255

Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr  
 260 265 270  
 Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly  
 275 280 285  
 Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn  
 290 295 300  
 Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met  
 305 310 315 320  
 Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile  
 325 330

&lt;210&gt; 645

&lt;211&gt; 1212

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1189)

&lt;223&gt; RXA00223

&lt;400&gt; 645

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 tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115  
 Met Arg Glu Val Ala  
 1 5  
 gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163  
 Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln  
 10 15 20  
 tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211  
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu  
 25 30 35  
 gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259  
 Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr  
 40 45 50  
 gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307  
 Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His  
 55 60 65  
 gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355  
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly  
 70 75 80 85  
 att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403  
 Ile Leu Glu Thr Val Lys Ala Leu Glu Gly Gly Ala Glu Ala Glu  
 90 95 100  
 ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451  
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu  
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc 499  
 Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr  
 120 125 130

ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc 547  
 Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser  
 135 140 145

ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg 595  
 Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro  
 150 155 160 165

gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac 643  
 Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His  
 170 175 180

aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca 691  
 Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser  
 185 190 195

cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc 739  
 Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile  
 200 205 210

cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca 787  
 Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Thr Ala Ala Ala  
 215 220 225

tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc 835  
 Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg  
 230 235 240 245

gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac 883  
 Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn  
 250 255 260

gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc 931  
 Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu  
 265 270 275

tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc 979  
 Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser  
 280 285 290

ttg cgg atc gaa gcc tcc aca ggt tcg gcc tgc tcc aac ggt gta aac  
 1027  
 Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn  
 295 300 305

cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc  
 1075  
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala  
 310 315 320 325

cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc  
 1123  
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser  
 330 335 340

atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt  
 1171

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg  
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg  
 1212

Thr Ala Gly Met Ala Phe  
 360

<210> 646

<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu  
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Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala  
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile  
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val  
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro  
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly  
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser  
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp  
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala  
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val  
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu  
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu  
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly  
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala  
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu  
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu

245	250	255
His Thr Ile Pro Asn Val Leu Val	His Thr Thr Glu Pro Ser Leu Pro	
260	265	270
Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile		
275	280	285
Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys		
290	295	300
Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile		
305	310	315
Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr		
325	330	335
Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val		
340	345	350
Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe		
355	360	

<210> 647  
 <211> 1197  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1174)  
 <223> RXN00262

<400> 647  
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 attctgtgca tgcacttgac ctaggactcg atattttcta atg ctc tac ctt gat 115  
 Met Leu Tyr Leu Asp  
 1 5  
 aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg 163  
 Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp  
 10 15 20  
 cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg 211  
 Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val  
 25 30 35  
 gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc 259  
 Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala  
 40 45 50  
 cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga 307  
 Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly  
 55 60 65  
 tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct 355  
 Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro  
 70 75 80 85



cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta	403
Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu	
90 95 100	
 gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac	451
Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr	
105 110 115	
 cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa	499
Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys	
120 125 130	
 gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat	547
Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn	
135 140 145	
 gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt	595
Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser	
150 155 160 165	
 acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac	643
Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp	
170 175 180	
 ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct	691
Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro	
185 190 195	
 aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc	739
Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile	
200 205 210	
 cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt	787
His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val	
215 220 225	
 gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa	835
Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu	
230 235 240 245	
 tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	883
Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro	
250 255 260	
 gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca	931
Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala	
265 270 275	
 tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg	979
Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu	
280 285 290	
 gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga	
1027	
Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly	
295 300 305	
 gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca	
1075	
Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala	
310 315 320 325	

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat  
1123

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
330 335 340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga  
1171

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg  
345 350 355

ggg tgacgctagt cagaggttta cgg

1197

Gly

<210> 648

<211> 358

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 648

Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala  
1 5 10 15

Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser  
20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala  
35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr  
50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala  
65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu  
85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu  
145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala  
165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His  
180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro  
195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser  
 210 215 220  
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu  
 225 230 235 240  
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu  
 245 250 255  
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg  
 260 265 270  
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr  
 275 280 285  
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser  
 290 295 300  
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu  
 305 310 315 320  
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr  
 325 330 335  
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala  
 340 345 350  
 Val Ala Leu Ile Arg Gly  
 355

<210> 649  
 <211> 920  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (79)..(897)  
 <223> FRXA00262

<400> 649  
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cgtgcttagc taatcctagtg gcc ggg cac ctc atc acc acc ccg atc gag 111  
 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu  
 1 5 10

cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159  
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
 15 20 25

ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207  
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
 30 35 40

gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255  
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
 45 50 55

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ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
60 65 70 75

gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
80 85 90

cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399
His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
95 100 105

aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
110 115 120

ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495
Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
125 130 135

ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
140 145 150 155

ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
160 165 170

gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
175 180 185

att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
190 195 200

gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
205 210 215

gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
220 225 230 235

gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
240 245 250

cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
255 260 265

gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920
Val Ala Leu Ile Arg Gly
270

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&lt;210&gt; 650

&lt;211&gt; 273

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 650

Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu  
 1 5 10 15

Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr  
 20 25 30

Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys  
 35 40 45

Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn  
 50 55 60

Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser  
 65 70 75 80

Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp  
 85 90 95

Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro  
 100 105 110

Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile  
 115 120 125

His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val  
 130 135 140

Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu  
 145 150 155 160

Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro  
 165 170 175

Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala  
 180 185 190

Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu  
 195 200 205

Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly  
 210 215 220

Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala  
 225 230 235 240

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
 245 250 255

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg  
 260 265 270

Gly

&lt;210&gt; 651

&lt;211&gt; 1296

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1273)

&lt;223&gt; RXN00435

&lt;400&gt; 651

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gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115
                               Val Gly Phe Asp Val
                               1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
                               10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
                               25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
                               40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
                               55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp
135 140 145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595
Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly
150 155 160 165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643
Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser
170 175 180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691
Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro
185 190 195

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ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739  
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly  
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787  
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser  
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835  
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser  
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883  
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His  
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg 931  
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly  
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979  
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser  
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc  
 1027  
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala  
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc  
 1075  
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe  
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac  
 1123  
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp  
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca  
 1171  
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala  
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg  
 1219  
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro  
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg  
 1267  
 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser  
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc  
 1296  
 Leu Ala  
 390

&lt;210&gt; 652

&lt;211&gt; 391

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 652

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Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly
  1           5           10           15

Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
      20           25           30

Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
      35           40           45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
      50           55           60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
      65           70           75           80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
      85           90           95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
      100          105          110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
      115          120          125

Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
      130          135          140

Glu Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala
      145          150          155          160

His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys
      165          170          175

Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr
      180          185          190

Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val
      195          200          205

Met Leu Asp Leu Gly Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile
      210          215          220

Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu
      225          230          235          240

Glu Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro
      245          250          255

Asn Leu Val Arg His Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val
      260          265          270

Val Glu Ala Met Gly Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu
      275          280          285

His Leu Val Glu Ser Leu Glu Gly Leu His Ala Val His Ile Val Gly
      290          295          300

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Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val  
 305 310 315 320  
 Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr  
 325 330 335  
 Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp  
 340 345 350  
 Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr  
 355 360 365  
 Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr  
 370 375 380  
 Arg Val Leu Ala Ser Leu Ala  
 385 390

&lt;210&gt; 653

&lt;211&gt; 638

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(615)

&lt;223&gt; FRXA00435

&lt;400&gt; 653

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Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu	
1 5 10 15	
tgg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg	96
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro	
20 25 30	
cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg	144
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu	
35 40 45	
gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg	192
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly	
50 55 60	
ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat	240
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp	
65 70 75 80	
gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc	288
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe	
85 90 95	
cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac	336
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His	
100 105 110	
gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc	384
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala	

115	120	125	
ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc acc atg gaa ggc gtg			432
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
130	135	140	
ccc gca gat atg gtg tac cgc cga ttg gtg gac aat cgt ttg atc act			480
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
145	150	155	160
acc gtc agc cct gct gac ccg ctg ctc gaa gca atg ggt gtg act gaa			528
Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu			
165	170		175
gct ggc gga tcg atc act atc gga cta agc ccg ttt agc acc tac tat			576
Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr			
180	185		190
gaa gtg gat cag ctg acc agg gtg ctg gca tcg ctt gcc taaaccgcaa			625
Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala			
195	200	205	
gcacgagctt gcc			638
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<213> <i>Corynebacterium glutamicum</i>			
<400> 654			
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Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro			
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Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu			
35	40		45
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly			
50	55		60
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp			
65	70	75	80
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe			
85	90		95
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His			
100	105		110
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala			
115	120		125
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
130	135		140
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
145	150	155	160

Thr	Val	Ser	Pro	Ala	Asp	Pro	Leu	Leu	Glu	Ala	Met	Gly	Val	Thr	Glu
				165					170					175	
Ala	Gly	Gly	Ser	Ile	Thr	Ile	Gly	Leu	Ser	Pro	Phe	Ser	Thr	Tyr	Tyr
			180					185					190		
Glu	Val	Asp	Gln	Leu	Thr	Arg	Val	Leu	Ala	Ser	Leu	Ala			
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<211> 535
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(535)  
<223> FRXA02801
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				Val	Gly	Phe	Asp	Val									5	
				1														
gcc agg gtt	cgg ggg ctt	tat acc tct	ttg ggc gat	ggc tgg acg	tac												163	
Ala Arg Val	Arg Gly Leu	Tyr Thr Ser	Leu Gly Asp	Gly Trp Thr	Tyr													
	10		15		20													
ctt aat tca	cat caa att	ccg cag gtt	ccg gag cgg	gtg gcg tcg	gga												211	
Leu Asn Ser	His Gln Ile	Pro Gln Val	Pro Glu Arg	Val Ala Ser	Gly													
	25		30		35													
gtt gcg gcg	gct ttc cgc	acg cat gcg	cag att tct	gag gtg acg	tcg												259	
Val Ala Ala	Ala Phe Arg	Thr His Ala	Gln Ile Ser	Glu Val Thr	Ser													
	40		45		50													
cag ccg att	gcg gtg gat	cag ttg gag	gct gct cgc	gag gca gtt	gcg												307	
Gln Pro Ile	Ala Val Asp	Gln Leu Glu	Ala Ala Arg	Glu Ala Val	Ala													
	55		60		65													
tcg ttg gcg	ggt gtg gat	ccg gac tgt	gtt gtg ctg	ggt ccc acg	agg												355	
Ser Leu Ala	Gly Val Asp	Pro Asp Cys	Val Val Leu	Gly Pro Thr	Arg													
	70		75		80		85											
cag ttt ttg	gct cat aca	ttg gcg cgc	ggg ttg ggt	ggg ttt gta	cgt												403	
Gln Phe Leu	Ala His Thr	Leu Ala Arg	Gly Leu Gly	Gly Phe Val	Arg													
	90		95		100													
cga aaa gcg	ggc gtg gtg	ttg tcg cgc	gcg gac gcg	gac tgg ctg	acc												451	
Arg Lys Ala	Gly Val Val	Leu Ser Arg	Ala Asp Ala	Asp Trp Leu	Thr													
	105		110		115													
gcg ccg ttc	cgc tcc ctc	gac ggc gtt	ttt agc tgg	gcc gag ccc	gat												499	
Ala Pro Phe	Arg Ser Leu	Asp Gly Val	Phe Ser Trp	Glu Pro Asp														
	120		125		130													
ttg ggc acc	ggc atg ctg	ccg gat tgg	cag tac cag													535		
Leu Gly Thr	Gly Met Leu	Pro Asp Trp	Gln Tyr Gln															

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135                                140                                145

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<212> PRT
<213> Corynebacterium glutamicum

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Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
                                20                                25                                30
Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
                                35                                40                                45
Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
  50                                55                                60
Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
  65                                70                                75                                80
Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
                                85                                90                                95
Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
                                100                                105                                110
Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
                                115                                120                                125
Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
  130                                135                                140

Gln
145

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<210> 657
<211> 1386
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1363)
<223> RXA02516
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aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc      115
                                         Met Ser Asp Phe Leu
                                           1                     5

aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca      163
Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro
                    10                      15                   20
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atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac	211
Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp	
25 30 35	
tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag	259
Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu	
40 45 50	
cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa	307
His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln	
55 60 65	
ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc	355
Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile	
70 75 80 85	
gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat	403
Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn	
90 95 100	
gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt	451
Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg	
105 110 115	
tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag	499
Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu	
120 125 130	
cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga	547
Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg	
135 140 145	
acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att	595
Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile	
150 155 160 165	
gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc	643
Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe	
170 175 180	
act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg	691
Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu	
185 190 195	
gtt cgt cgt gcc aag gct gtc ggc gct ctc acg gtg ctt gat gcg tgc	739
Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys	
200 205 210	
cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat	787
Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp	
215 220 225	
ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca ggc gtg ggc	835
Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly	
230 235 240 245	
gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg	883
Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu	
250 255 260	
act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac	931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr  
 265 270 275  
 gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979  
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln  
 280 285 290  
 gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg  
 1027  
 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met  
 295 300 305  
 gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa  
 1075  
 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu  
 310 315 320 325  
 aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca  
 1123  
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala  
 330 335 340  
 gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca  
 1171  
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro  
 345 350 355  
 cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc  
 1219  
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val  
 360 365 370  
 ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg  
 1267  
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser  
 375 380 385  
 aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac  
 1315  
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp  
 390 395 400 405  
 cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag  
 1363  
 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu  
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 1386  
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Leu	Ala	Tyr	Leu	Asp	Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val															
		35					40					45																		
Trp	Arg	Ala	Glu	Glu	His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His															
	50					55					60																			
Arg	Gly	Ala	Tyr	Gln	Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly															
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Ala	Arg	Glu	Lys	Ile	Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile															
			85						90					95																
Ala	Phe	Thr	Lys	Asn	Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr															
		100					105						110																	
Leu	Gly	Asp	Asp	Arg	Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr															
	115					120					125																			
Val	Val	Ile	Thr	Glu	Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln															
	130					135					140																			
Glu	Leu	Cys	Arg	Arg	Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr															
145					150					155				160																
Glu	Asp	Gly	Arg	Ile	Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val															
			165						170					175																
Lys	Val	Val	Ala	Phe	Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala															
		180					185					190																		
Asp	Val	Pro	Glu	Leu	Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr															
	195					200					205																			
Val	Leu	Asp	Ala	Cys	Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His															
	210				215						220																			
Glu	Leu	Asp	Val	Asp	Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly															
225				230						235				240																
Pro	Ala	Gly	Val	Gly	Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu															
			245					250					255																	
Leu	Pro	Pro	Phe	Leu	Thr	Gly	Gly	Ser	Met	Ile	Glu	Val	Val	Thr	Met															
		260					265					270																		
Glu	Gly	Ser	Thr	Tyr	Ala	Ala	Ala	Pro	Gln	Arg	Phe	Glu	Ala	Gly	Thr															
	275					280					285																			
Gln	Met	Thr	Ser	Gln	Val	Val	Gly	Leu	Gly	Ala	Ala	Val	Asp	Met	Leu															
	290				295						300																			
Asn	Glu	Ile	Gly	Met	Glu	Ala	Ile	Ala	Ala	His	Glu	His	Ala	Leu	Thr															
305				310						315				320																
Ala	Tyr	Ala	Leu	Glu	Lys	Leu	Thr	Ala	Ile	Lys	Gly	Leu	Thr	Ile	Ala															
			325					330					335																	
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				Met	Asn	Leu	Glu	Gln									
					1			5									
atg	tac	cag	gag	gtg	atc	ctg	gac	cac	tac	aaa	aac	cca	cag	cac	aag		163
Met	Tyr	Gln	Glu	Val	Ile	Leu	Asp	His	Tyr	Lys	Asn	Pro	Gln	His	Lys		
				10					15					20			
ggc	ctt	cgg	gat	cct	ttc	gat	gct	gag	gtt	cac	cac	gtc	aac	cct	tct		211
Gly	Leu	Arg	Asp	Pro	Phe	Asp	Ala	Glu	Val	His	His	Val	Asn	Pro	Ser		
			25					30					35				
tgt	ggc	gac	gaa	ttg	act	ctg	cgc	gtg	aag	ctg	tct	gag	gac	ggc	tcc		259
Cys	Gly	Asp	Glu	Leu	Thr	Leu	Arg	Val	Lys	Leu	Ser	Glu	Asp	Gly	Ser		
		40					45					50					
acc	gtg	gag	gac	gtc	tcc	tac	gaa	gca	gtt	ggc	tgc	tca	atc	agc	cag		307
Thr	Val	Glu	Asp	Val	Ser	Tyr	Glu	Ala	Val	Gly	Cys	Ser	Ile	Ser	Gln		
		55				60					65						
gcc	tcc	acg	tcc	gtt	atg	gcc	gag	gag	atc	gtg	ggc	caa	ccc	gtc	gac		355
Ala	Ser	Thr	Ser	Val	Met	Ala	Glu	Glu	Ile	Val	Gly	Gln	Pro	Val	Asp		
	70				75				80						85		
aag	gcg	ctg	gaa	aag	ctc	aca	gaa	ttt	gag	aag	atg	atc	gtt	tcc	cgc		403
Lys	Ala	Leu	Glu	Lys	Leu	Thr	Glu	Phe	Glu	Lys	Met	Ile	Val	Ser	Arg		
				90				95					100				
ggt	cag	ttt	gtt	ggc	gat	gaa	gat	ctc	atc	gga	gat	ggc	gtt	gct	ttc		451
Gly	Gln	Phe	Val	Gly	Asp	Glu	Asp	Leu	Ile	Gly	Asp	Gly	Val	Ala	Phe		
			105					110					115				



tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499  
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly  
           120                          125                          130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547  
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His  
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<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

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Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His  
                           20                          25                          30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu  
                           35                          40                          45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly  
           50                          55                          60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val  
           65                          70                          75                          80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys  
                           85                          90                          95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly  
                           100                          105                          110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys  
           115                          120                          125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala  
           130                          135                          140

Val Ala His Ala His  
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<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01747

<400> 661

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	Val Thr Ile Ala Pro	
	1 5	
gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg	163	
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro		
	10 15 20	
att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct	211	
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro		
	25 30 35	
gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act	259	
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr		
	40 45 50	
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc	307	
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser		
	55 60 65	
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt	355	
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys		
	70 75 80 85	
gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt	403	
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly		
	90 95 100	
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac	451	
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr		
	105 110 115	
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca	499	
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala		
	120 125 130	
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac	547	
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His		
	135 140 145	
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg	595	
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu		
	150 155 160 165	
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643	
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val		
	170 175 180	
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691	
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr		
	185 190 195	
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739	
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val		
	200 205 210	
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787	
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile		
	215 220 225	

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835  
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr  
 230 235 240 245

atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883  
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg  
 250 255 260

tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931  
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu  
 265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979  
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr  
 280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa  
 1027  
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu  
 295 300 305

atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc  
 1075  
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr  
 310 315 320 325

gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac  
 1123  
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp  
 330 335 340

acc cca gtg gtg tcc ttc aac taagcccgaa gttttttaac cgc  
 1167  
 Thr Pro Val Val Ser Phe Asn  
 345

<210> 662

<211> 348

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 662

Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg  
 1 5 10 15

Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln  
 20 25 30

Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly  
 35 40 45

Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His  
 50 55 60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn  
 65 70 75 80

Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu  
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu  
 100 105 110  
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu  
 115 120 125  
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His  
 130 135 140  
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser  
 145 150 155 160  
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val  
 165 170 175  
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg  
 180 185 190  
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg  
 195 200 205  
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu  
 210 215 220  
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly  
 225 230 235 240  
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe  
 245 250 255  
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala  
 260 265 270  
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu  
 275 280 285  
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu  
 290 295 300  
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr  
 305 310 315 320  
 Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr  
 325 330 335  
 Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn  
 340 345

&lt;210&gt; 663

&lt;211&gt; 876

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXA01746

&lt;400&gt; 663

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tgacttatca accttgtag ggctagggtg gatatctatc atg act gca cca aga	115
Met Thr Ala Pro Arg	
1 5	
gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc	163
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro	
10 15 20	
att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat	211
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp	
25 30 35	
tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat	259
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp	
40 45 50	
cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc	307
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg	
55 60 65	
acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct	355
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala	
70 75 80 85	
gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc	403
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile	
90 95 100	
tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta	451
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val	
105 110 115	
aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt	499
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val	
120 125 130	
gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct	547
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala	
135 140 145	
cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata	595
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile	
150 155 160 165	
act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg	643
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr	
170 175 180	
ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc	691
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly	
185 190 195	
ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa	739
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu	
200 205 210	
tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg	787
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg	
215 220 225	

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835  
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys  
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876  
 Asn Leu Pro Lys Arg Gly  
 250

<210> 664

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 664

Met Thr Ala Pro Arg Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg  
 1 5 10 15

Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr  
 20 25 30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn  
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr  
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu  
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro  
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp  
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val  
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly  
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala  
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile  
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly  
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp  
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp  
 210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala  
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly

245

250

<210> 665  
 <211> 1179  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1156)  
 <223> RXA02106

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 aagcaaaatc tcttttagcaa attcggttac tgtggggcgc atg aat aac cat ttt 115  
 Met Asn Asn His Phe  
 1 5  
 gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc 163  
 Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr  
 10 15 20  
 gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc 211  
 Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu  
 25 30 35  
 gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg 259  
 Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala  
 40 45 50  
 tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gga gcg 307  
 Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala  
 55 60 65  
 ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat 355  
 Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp  
 70 75 80 85  
 att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc 403  
 Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr  
 90 95 100  
 gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt 451  
 Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu  
 105 110 115  
 aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag 499  
 Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln  
 120 125 130  
 cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg 547  
 Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val  
 135 140 145  
 atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt 595  
 Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val  
 150 155 160 165  
 aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt ggc ggt gca 643

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Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala
      170                      175                      180

atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg   691
Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro
      185                      190                      195

gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg   739
Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu
      200                      205                      210

gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg   787
Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp
      215                      220                      225

tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc   835
Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly
      230                      235                      240                      245

gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg   883
Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met
      250                      255                      260

tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga   931
Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly
      265                      270                      275

aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt   979
Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val
      280                      285                      290

gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac
1027
Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp
      295                      300                      305

acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag
1075
Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu
      310                      315                      320                      325

ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa
1123
Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys
      330                      335                      340

tac gcc acc gag gag tgg act aag cga gtt caa tagtttctat ggatctgcac
1176
Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
      345                      350

aag
1179

<210> 666
<211> 352
<212> PRT
<213> Corynebacterium glutamicum

<400> 666

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Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val  
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 Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser  
 20 25 30  
 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg  
 35 40 45  
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala  
 50 55 60  
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly  
 65 70 75 80  
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly  
 85 90 95  
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val  
 100 105 110  
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln  
 115 120 125  
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp  
 130 135 140  
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile  
 145 150 155 160  
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met  
 165 170 175  
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr  
 180 185 190  
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln  
 195 200 205  
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His  
 210 215 220  
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly  
 225 230 235 240  
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu  
 245 250 255  
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln  
 260 265 270  
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser  
 275 280 285  
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg  
 290 295 300  
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly  
 305 310 315 320  
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp

325 330 335

Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln

340 345 350

<210> 667  
<211> 403  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(403)
<223> RXS01183
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<400> 667																
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Met Ala Phe Ser Val 1 5																
gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163																
Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln 10 15 20																
tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211																
Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu 25 30 35																
gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259																
Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala 40 45 50																
ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307																
Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val 55 60 65																
ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac 355																
Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn 70 75 80 85																
gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403																
Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala Glu Glu Glu Glu Pro 90 95 100																

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<210> 668
<211> 101
<212> PRT
<213> Corynebacterium glutamicum
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<400> 668  
Met Ala Phe Ser Val Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu  
1 5 10 15  
Gly Thr Ile Thr Gln Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val

20					25					30						
Asp	Glu	Pro	Leu	Leu	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	
35					40					45						
Pro	Ser	Pro	Val	Ala	Gly	Val	Ile	Leu	Glu	Ile	Lys	Ala	Glu	Glu	Asp	
50					55					60						
Asp	Thr	Val	Asp	Val	Gly	Gly	Val	Ile	Ala	Ile	Ile	Gly	Asp	Ala	Asp	
65					70					75					80	
Glu	Thr	Pro	Ala	Asn	Glu	Ala	Pro	Ala	Asp	Glu	Ala	Pro	Ala	Pro	Ala	
85					90					95						
Glu	Glu	Glu	Glu	Pro												
100																

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<210> 669
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1282)
<223> RXS01260
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Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu			
120	125	130	
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag			547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys			
135	140	145	
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg			595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg			
150	155	160	165
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac			643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp			
	170	175	180
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc			691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe			
	185	190	195
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc			739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu			
	200	205	210
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc			787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val			
	215	220	225
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct			835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala			
	230	235	240
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt			883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly			
	250	255	260
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc			931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr			
	265	270	275
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc			979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala			
	280	285	290
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc			
1027			
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe			
	295	300	305
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca			
1075			
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala			
	310	315	320
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg			
1123			
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu			
	330	335	340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag  
1171

Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln  
345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac  
1219

Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His  
360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga  
1267

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly  
375 380 385

cac atg atc aac ttc tagaatccac ctcgttgccc ctg  
1305

His Met Ile Asn Phe  
390

<210> 670

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser  
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Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile  
20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu  
35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys  
50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe  
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala  
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe  
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe  
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile  
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala  
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln  
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180							185					190				
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn	
		195					200					205				
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr	
	210					215					220					
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala	
225					230					235					240	
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala	
				245					250					255		
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met	
			260					265					270			
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr	
		275					280					285				
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val	
	290					295					300					
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu	
305					310					315					320	
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu	
				325				330						335		
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu	
			340					345					350			
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg	
		355					360					365				
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala	
	370					375					380					
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe							
385					390											

```
<210> 671
<211> 294
<212> DNA
<213> Corynebacterium glutamicum
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```
<220>  
<221> CDS  
<222> (101)..(271)  
<223> RXS01261
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<400> 671  
gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60

atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115  
Val Thr Glu His Tyr  
1 5

gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163  
Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile

```

                10                15                20
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
                25                30                35

tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
                40                45                50

gat caa aaa cgc tgaagttgcc cataccttta ccc 294
Asp Gln Lys Arg
                55

```

<210> 672  
 <211> 57  
 <212> PRT  
 <213> Corynebacterium glutamicum

```

<400> 672
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
  1                      5                      10                      15

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
                20                25                30

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
                35                40                45

Pro Ser Lys Val Ser Asp Gln Lys Arg
                50                55

```

<210> 673  
 <211> 1005  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(982)  
 <223> RXA02717

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<400> 673
aggcatgtcc ctaacgaaca tcccagcctc atctcaatgg gcaattagcg acgttttgaa 60

gcgtccttca cccggccgag tacctttttc tgtcgagttt atg cca ccc cgc gac 115
                                Met Pro Pro Arg Asp
                                1                      5

gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac 163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp
                10                15                20

ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc 211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr
                25                30                35

cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg 259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu

```

40	45	50	
acc act ctg gtg cac ctg	acc ctg gtt aac cac act	cgc gaa gag atg	307
Thr Thr Leu Val His Leu	Thr Leu Val Asn His Thr	Arg Glu Glu Met	
55	60	65	
aag gca att ctt cgg gaa tac cta	gag ctg gga tta aca aac ctg ttg		355
Lys Ala Ile Leu Arg Glu Tyr Leu	Glu Leu Gly Leu Thr Asn Leu Leu		
70	75	80	85
gcg ctt cga gga gat ccg cct gga	gac cca tta ggc gat tgg gtg agc		403
Ala Leu Arg Gly Asp Pro Pro Gly	Asp Pro Leu Gly Asp Trp Val Ser		
90	95	100	
acc gat gga gga ctg aac tat gcc	tct gag ctc atc gat ctt att aag		451
Thr Asp Gly Gly Leu Asn Tyr Ala	Ser Glu Leu Ile Asp Leu Ile Lys		
105	110	115	
tcc act cct gag ttc cgg gaa ttc	gac ctc ggt atc gcc tcc ttc ccc		499
Ser Thr Pro Glu Phe Arg Glu Phe	Asp Leu Gly Ile Ala Ser Phe Pro		
120	125	130	
gaa ggg cat ttc cgg gcg aaa act	cta gaa gaa gac acc aaa tac act		547
Glu Gly His Phe Arg Ala Lys Thr	Leu Glu Glu Asp Thr Lys Tyr Thr		
135	140	145	
ctg gcg aag ctg cgt gga ggg gca	gag tac tcc atc acg cag atg ttc		595
Leu Ala Lys Leu Arg Gly Gly Ala	Glu Tyr Ser Ile Thr Gln Met Phe		
150	155	160	165
ttt gat gtg gaa gac tac ctg cga	ctt cgt gat cgc ctt gtc gct gca		643
Phe Asp Val Glu Asp Tyr Leu Arg	Leu Arg Asp Arg Leu Val Ala Ala		
170	175	180	
gac ccc att cat ggt gcg aag cca	atc att cct ggc atc atg ccc att		691
Asp Pro Ile His Gly Ala Lys Pro	Ile Ile Pro Gly Ile Met Pro Ile		
185	190	195	
acg agc ctg cgg tct gtg cgt cga	cag gtc gaa ctc tct ggt gct caa		739
Thr Ser Leu Arg Ser Val Arg Arg	Gln Val Glu Leu Ser Gly Ala Gln		
200	205	210	
ttg ccg agc caa cta gaa gaa tca	ctt gtt cga gct gca aac ggc aat		787
Leu Pro Ser Gln Leu Glu Glu Ser	Leu Val Arg Ala Ala Asn Gly Asn		
215	220	225	
gaa gaa gcg aac aaa gac gag atc	cgc aag gtg ggc att gaa tat tcc		835
Glu Glu Ala Asn Lys Asp Glu Ile	Arg Lys Val Gly Ile Glu Tyr Ser		
230	235	240	245
acc aat atg gca gag cga ctc att	gcc gaa ggt gcg gaa gat ctg cac		883
Thr Asn Met Ala Glu Arg Leu Ile	Ala Glu Gly Ala Glu Asp Leu His		
250	255	260	
ttc atg acg ctt aac ttc acc cgt	gca acc caa gaa gtg ttg tac aac		931
Phe Met Thr Leu Asn Phe Thr Arg	Ala Thr Gln Glu Val Leu Tyr Asn		
265	270	275	
ctt ggc atg gcg cct gct tgg gga	gca gag cac ggc caa gac gcg gtg		979
Leu Gly Met Ala Pro Ala Trp Gly	Ala Glu His Gly Gln Asp Ala Val		
280	285	290	



cgt taagccctct taggaatcat gaa  
 1005  
 Arg

<210> 674  
 <211> 294  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 674  
 Met Pro Pro Arg Asp Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala  
   1                  5                  10                  15  
 Glu Val Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly  
           20                  25                  30  
 Ala Gly Gly Ser Thr Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu  
           35                  40                  45  
 Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His  
           50                  55                  60  
 Thr Arg Glu Glu Met Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly  
   65                  70                  75                  80  
 Leu Thr Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu  
                   85                  90                  95  
 Gly Asp Trp Val Ser Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu  
           100                  105                  110  
 Ile Asp Leu Ile Lys Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly  
           115                  120                  125  
 Ile Ala Ser Phe Pro Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu  
           130                  135                  140  
 Asp Thr Lys Tyr Thr Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser  
  145                  150                  155                  160  
 Ile Thr Gln Met Phe Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp  
           165                  170                  175  
 Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro  
           180                  185                  190  
 Gly Ile Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu  
           195                  200                  205  
 Leu Ser Gly Ala Gln Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg  
           210                  215                  220  
 Ala Ala Asn Gly Asn Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val  
  225                  230                  235                  240  
 Gly Ile Glu Tyr Ser Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly  
           245                  250                  255

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln  
260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His  
275 280 285

Gly Gln Asp Ala Val Arg  
290

```
<210> 675
<211> 601
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(601)  
<223> RXN02027
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<400> 675  
tcacgtgctc atcgataggg aaactcatgg aaccaagagt acctgcccc qcaaccccaa 60

tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115  
Met Ser Gln Thr Lys  
1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163  
Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu  
10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211  
Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr  
25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259  
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val  
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctg cac gcc gaa    307  
Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu

55                  60                  65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355  
Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp  
70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403  
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly  
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451  
Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe  
105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499  
Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile  
120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547  
Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

```

      135              140              145
gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
150              155              160              165

gat atc
Asp Ile
601

```

```

<210> 676
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 676
Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1              5              10              15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
      20              25              30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
      35              40              45

Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
      50              55              60

Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
      65              70              75              80

Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
      85              90              95

Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
      100             105             110

Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
      115             120             125

Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
      130             135             140

Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
      145             150             155             160

Gly Glu Ile Arg Asp Asp Ile
      165

```

```

<210> 677
<211> 595
<212> DNA
<213> Corynebacterium glutamicum

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```

<220>
<221> CDS
<222> (101)..(595)
<223> FRXA02027

```

&lt;400&gt; 677

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tcacgtgctc atcgataggc aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60

tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
                                         Met Ser Gln Thr Lys
                                         1      5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
              10              15              20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
              25              30              35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
              40              45              50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
              55              60              65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
              70              75              80              85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
              90              95              100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
              105              110              115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
              120              125              130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
Arg Leu Gly Lys Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
              135              140              145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
              150              155              160              165

```

&lt;210&gt; 678

&lt;211&gt; 165

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 678

```

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1              5              10              15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20              25              30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala

```

35	40	45
Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp		
50	55	60
Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu		
65	70	75
Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val		
85	90	95
Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro		
100	105	110
Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys		
115	120	125
Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg		
130	135	140
Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn		
145	150	155
Gly Glu Ile Arg Asp		
165		

&lt;210&gt; 679

&lt;211&gt; 579

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(556)

&lt;223&gt; RXA00106

&lt;400&gt; 679

```

tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg 60
gctacgatcc acaccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
                                     Met Ile Gly Ala Ile
                                     1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
                                     10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
                                     25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
                                     40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
                                     55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355

```

```

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70                      75                      80                      85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc    403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
                      90                      95                      100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act    451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
                      105                      110                      115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa    499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
                      120                      125                      130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac    547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
                      135                      140                      145

atc aag gtt taaggagcaa acaacatgag caa    579
Ile Lys Val
150

<210> 680
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 680
Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
 1                      5                      10                      15

Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
                20                      25                      30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
                35                      40                      45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
                50                      55                      60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
        65                      70                      75                      80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
                85                      90                      95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
                100                      105                      110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
                115                      120                      125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
                130                      135                      140

Lys Phe Gln Arg Tyr Ile Lys Val
145                      150

```

```
<210> 681
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1021)
<223> RXN01321
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<400> 681																
ggagggtgta gtcaaggatt tgggccatgg tggagcggga aatcgtcata tccataccct 60																
acttagacct gacttagtgt gggaaaattht ccagggtaga atg caa cga atg acc 115																
Met Gln Arg Met Thr 5																
ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163																
Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu 20																
cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg 211																
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val 35																
gcg aag ttg tct tct ttc cta gct gag cgt ggg ggt tgg att act gag 259																
Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu 50																
gct gga tat ttc acg gat cct gat tct aat tgg ttc ttt act cgt cag 307																
Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp Phe Phe Thr Arg Gln 65																
gcg att cgc gct gag tct att gat acc acg att gag cag ttg cgg gag 355																
Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile Glu Gln Leu Arg Glu 85																
gag ttc gct ccg ctt gcg gag gag ttc ggc ccg agg gct aag tgg agt 403																
Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro Arg Ala Lys Trp Ser 100																
ttc act gac act gcg cag gtg aag aag gct gtg ttg ttg gtg tct aag 451																
Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val Leu Leu Val Ser Lys 115																
gag ggc cac tgc ttg cac gat ttg tta ggt cgt gtg gct gag aat gat 499																
Glu Gly His Cys Leu His Asp Leu Leu Gly Arg Val Ala Glu Asn Asp 130																
tat ccg atg gaa gtt gtt gcg gtt gtg ggt aac cat gag aac ttg cgt 547																
Tyr Pro Met Glu Val Val Ala Val Val Gly Asn His Glu Asn Leu Arg 145																
tat att gcg gag aac cat aat gtt ccg ttt ttc cat gtg ccg ttt cct 595																
Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe His Val Pro Phe Pro 165																
aag gat gcg gtt ggt aag cgg aag gcg ttt gac cag gtc gct gag att 643																
Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile 180																

gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691  
 Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln  
                   185                                  190                                  195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739  
 Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn  
                   200                                  205                                  210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787  
 Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His  
                   215                                  220                                  225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835  
 Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr  
 230                                  235                                  240                                  245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883  
 Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile  
                                   250                                  255                                  260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931  
 Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg  
                                   265                                  270                                  275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979  
 Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu  
                   280                                  285                                  290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat  
 1021  
 Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp  
                   295                                  300                                  305

taaggctttt tgcttttcga cgc  
 1044

<210> 682

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 682

Met Gln Arg Met Thr Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser  
   1                                  5                                  10                                  15

Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp  
                   20                                  25                                  30

Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly  
                   35                                  40                                  45

Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp  
                   50                                  55                                  60

Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile  
   65                                  70                                  75                                  80

Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro  
                   85                                  90                                  95



Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val  
 100 105 110  
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg  
 115 120 125  
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn  
 130 135 140  
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe  
 145 150 155 160  
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp  
 165 170 175  
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu  
 180 185 190  
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala  
 195 200 205  
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly  
 210 215 220  
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
 225 230 235 240  
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
 245 250 255  
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met  
 260 265 270  
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu  
 275 280 285  
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val  
 290 295 300  
 Val Phe Asp  
 305

&lt;210&gt; 683

&lt;211&gt; 582

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (23) ..(559)

&lt;223&gt; FRXA01321

&lt;400&gt; 683

cttgcacgat ttgttaggtc gtgtg gct gag aat gat tat ccg atg gaa gtt 52  
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val  
 1 5 10  
 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100  
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn  
 15 20 25

```

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148
His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly
      30              35              40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196
Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp
      45              50              55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244
Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp
      60              65              70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292
Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe
      75              80              85              90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340
Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg
      95              100              105

ggg gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388
Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu
      110              115              120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436
Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys
      125              130              135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484
Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln
      140              145              150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
      155              160              165              170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
Tyr Gly Asn Arg Thr Val Val Phe Asp
      175

cgc 582

```

&lt;210&gt; 684

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 684

```

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
  1              5              10              15

```

```

His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
      20              25              30

```

```

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
      35              40              45

```

```

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
      50              55              60

```

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala  
65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly  
85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met  
130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu  
145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val  
165 170 175

Val Phe Asp

<210> 685  
<211> 975  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(952)  
<223> RXA00461

<400> 685  
tggtgggagg gatgacagga ttgtcgaaga taacgtgaag tgggtgttcc ggcattgtgtt 60

tgattgtaag gccttggaag aggggtggaat aatagcgggc gtg act gca atc aaa 115  
Val Thr Ala Ile Lys  
1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163  
Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln  
10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211  
Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr  
25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259  
Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys  
40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307  
His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu  
55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355  
Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct	403			
Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro				
90	95	100		
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag	451			
Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys				
105	110	115		
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac	499			
Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn				
120	125	130		
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg	547			
Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu				
135	140	145		
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc	595			
Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly				
150	155	160		
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt	643			
Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg				
170	175	180		
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg	691			
Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu				
185	190	195		
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag	739			
Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln				
200	205	210		
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc	787			
Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu				
215	220	225		
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac	835			
Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His				
230	235	240		
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc	883			
Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly				
250	255	260		
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc	931			
Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg				
265	270	275		
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg	975			
Ala Glu Lys Leu Ala Gly Leu				
280				

&lt;210&gt; 686

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 686

Val Thr Ala Ile Lys Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe  
 1 5 10 15  
 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val  
 20 25 30  
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser  
 35 40 45  
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser  
 50 55 60  
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala  
 65 70 75 80  
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val  
 85 90 95  
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg  
 100 105 110  
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly  
 115 120 125  
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly  
 130 135 140  
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys  
 145 150 155 160  
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu  
 165 170 175  
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr  
 180 185 190  
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile  
 195 200 205  
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro  
 210 215 220  
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu  
 225 230 235 240  
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser  
 245 250 255  
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His  
 260 265 270  
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu  
 275 280

&lt;210&gt; 687

&lt;211&gt; 711

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(688)

&lt;223&gt; RXA01514

&lt;400&gt; 687

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accacagaaa tgcctgtcgt tccagatcag cccatcgatg gtgattccgg gaagtcgcgt 60

gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115
Val Asp Asn His Ala
1 5

gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
10 15 20

ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
25 30 35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
40 45 50

cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
55 60 65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
70 75 80 85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
90 95 100

ggg aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
105 110 115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
120 125 130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
135 140 145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
150 155 160 165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
170 175 180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
185 190 195

taaataaacg taccctcttt gac 711

```

&lt;210&gt; 688

&lt;211&gt; 196

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 688

Val Asp Asn His Ala Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr  
 1 5 10 15

Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg  
 20 25 30

Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu  
 35 40 45

Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr  
 50 55 60

Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile  
 65 70 75 80

Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His  
 85 90 95

Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys  
 100 105 110

Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu  
 115 120 125

Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala  
 130 135 140

Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met  
 145 150 155 160

Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg  
 165 170 175

Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu  
 180 185 190

Ile Arg Gly His  
 195

&lt;210&gt; 689

&lt;211&gt; 513

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(490)

&lt;223&gt; RXA01516

&lt;400&gt; 689

tctgcacata tgggagcatg ggggtgtgcgc gtgcacgatg tcccagtatc aagggacgct 60

gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115

```

Met Ala Asp Arg Ile
1 5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
10 15 20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
25 30 35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
40 45 50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
55 60 65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
70 75 80 85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
90 95 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
105 110 115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
120 125 130

agttttgtcc atc 513

```

&lt;210&gt; 690

&lt;211&gt; 130

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 690

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Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
1 5 10 15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
20 25 30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
35 40 45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
85 90 95

```



Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val  
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser  
 115 120 125

Asn Ala  
 130

<210> 691

<211> 975

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 691

taagcctggt gctgtgacca cgacgtctgc ggtgcgcggc ggttttaaga acaacgctgc 60

ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115  
 Met Asn Val Ser Ser  
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163  
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211  
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala  
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259  
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp  
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307  
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser  
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355  
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala  
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403  
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala  
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451  
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu  
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499  
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val  
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln  
 135 140 145  
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595  
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp  
 150 155 160 165  
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643  
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile  
 170 175 180  
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691  
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp  
 185 190 195  
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739  
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile  
 200 205 210  
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787  
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp  
 215 220 225  
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835  
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala  
 230 235 240 245  
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883  
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His  
 250 255 260  
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931  
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg  
 265 270 275  
 agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975  
 Ser Gly Gly Thr His His Gly  
 280

&lt;210&gt; 692

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 692

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly  
 1 5 10 15  
 Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile  
 20 25 30  
 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly  
 35 40 45  
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val  
 50 55 60  
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys  
 65 70 75 80

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu  
115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser  
195 200 205

Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala  
210 215 220

Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
225 230 235 240

Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp  
245 250 255

Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val  
260 265 270

Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly  
275 280

&lt;210&gt; 693

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(859)

&lt;223&gt; RXA02024

&lt;400&gt; 693

cactgatgac ctggatcagg ccgtcaaatt catcgctgat gcacacgctg gattggacgt 60

agcgcgtctc cacaattaag cagtggctac attaggtgtt atg agt tct ttg ccg 115  
Met Ser Ser Leu Pro  
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163  
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys  
10 15 20

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg cgg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
230 235 240 245	
cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	

&lt;210&gt; 694

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 694

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Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
 1             5             10             15

Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
      20             25             30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
      35             40             45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50             55             60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
65             70             75             80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
      85             90             95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
      100            105            110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
      115            120            125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
      130            135            140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
145            150            155            160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
      165            170            175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
      180            185            190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
      195            200            205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
      210            215            220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
225            230            235            240

Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr
      245            250

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&lt;210&gt; 695

&lt;211&gt; 579

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(556)

&lt;223&gt; RXA00106

&lt;400&gt; 695

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gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115  
 Met Ile Gly Ala Ile  
 1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro  
 10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly  
 25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259  
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys  
 40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307  
 Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly  
 55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355  
 Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly  
 70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403  
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala  
 90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451  
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr  
 105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499  
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu  
 120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547  
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr  
 135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579  
 Ile Lys Val  
 150

&lt;210&gt; 696

&lt;211&gt; 152

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 696

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp  
 1 5 10 15

Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys  
                   20                  25                  30  
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu  
                   35                  40                  45  
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser  
                   50                  55                  60  
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
                   65                  70                  75                  80  
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
                   85                  90                  95  
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
                   100                  105                  110  
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
                   115                  120                  125  
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr  
                   130                  135                  140  
 Lys Phe Gln Arg Tyr Ile Lys Val  
                   145                  150

<210> 697  
 <211> 1556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1533)  
 <223> RXA00989

<400> 697  
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 Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn  
   1                  5                  10                  15  
 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96  
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser  
                   20                  25                  30  
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144  
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu  
                   35                  40                  45  
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192  
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu  
                   50                  55                  60  
 gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240  
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met  
   65                  70                  75                  80  
 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288  
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

85										90					95					
att	cac	gtg	gct	ggc	acc	aac	ggg	aag	acc	tcc	acc	acc	cgc	atg	atc	336				
Ile	His	Val	Ala	Gly	Thr	Asn	Gly	Lys	Thr	Ser	Thr	Thr	Arg	Met	Ile					
100										105					110					
gag	tcg	ttg	ctg	cgc	gca	ttc	cac	cgc	cgc	acc	ggc	cgg	acc	acc	agc	384				
Glu	Ser	Leu	Leu	Arg	Ala	Phe	His	Arg	Arg	Thr	Gly	Arg	Thr	Thr	Ser					
115										120					125					
ccg	cac	ctg	cag	ctg	gta	acc	gaa	cgc	atc	gcg	att	gat	ggc	aag	ccc	432				
Pro	His	Leu	Gln	Leu	Val		Glu	Arg	Ile	Ala	Ile	Asp	Gly	Lys	Pro					
130										135					140					
atc	cac	ccg	cgt	gat	ttc	gtg	cgg	atc	tac	gaa	gag	att	aag	ccc	tac	480				
Ile	His	Pro	Arg	Asp	Phe	Val	Arg	Ile	Tyr	Glu	Glu	Ile	Lys	Pro	Tyr					
145										150					155					160
atg	gag	atg	acc	gac	gcc	tgg	tca	gag	gcc	gag	ggc	gga	ccg	aag	atg	528				
Met	Glu	Met	Thr	Asp	Ala	Trp	Ser	Glu	Ala	Glu	Gly	Gly	Pro	Lys	Met					
165										170					175					
agc	aag	ttt	gag	gca	ctc	gtg	gcc	ctc	gct	tac	gca	ggg	ttt	gcc	gac	576				
Ser	Lys	Phe	Glu	Ala	Leu	Val	Ala	Leu	Ala	Tyr	Ala	Gly	Phe	Ala	Asp					
180										185					190					
gct	cct	gtt	gac	gtc	gcc	gtc	gtt	gag	gtt	ggg	ctt	ggc	gga	cgc	tgg	624				
Ala	Pro	Val	Asp	Val	Ala	Val	Val	Glu	Val	Gly	Leu	Gly	Gly	Arg	Trp					
195										200					205					
gat	gcc	act	aac	gtg	atc	aac	gca	gct	gtt	tcc	gtg	atc	acc	ccg	gtg	672				
Asp	Ala	Thr	Asn	Val	Ile	Asn	Ala	Ala	Val	Ser	Val	Ile	Thr	Pro	Val					
210										215					220					
ggc	atg	gac	cac	gtg	gat	cgc	ctg	ggc	aac	acc	att	ggg	gaa	atc	gct	720				
Gly	Met	Asp	His	Val	Asp	Arg	Leu	Gly	Asn	Thr	Ile	Gly	Glu	Ile	Ala					
225										230					235					240
ggg	gaa	aag	gcc	ggc	atc	atc	aag	gct	cgt	cct	gca	tct	gag	gat	ggc	768				
Gly	Glu	Lys	Ala	Gly	Ile	Ile	Lys	Ala	Arg	Pro	Ala	Ser	Glu	Asp	Gly					
245										250					255					
acc	gag	cct	gag	ggc	aac	gtt	gtc	atc	gtg	ggc	aag	cag	gag	cca	gaa	816				
Thr	Glu	Pro	Glu	Gly	Asn	Val	Val	Ile	Val	Gly	Lys	Gln	Glu	Pro	Glu					
260										265					270					
gca	atg	aac	gtg	att	ctg	cag	caa	gcc	gtg	gac	gtg	gac	gca	gct	gtt	864				
Ala	Met	Asn	Val	Ile	Leu	Gln	Gln	Ala	Val	Asp	Val	Asp	Ala	Ala	Val					
275										280					285					
gct	cgt	ttg	aac	atg	gaa	ttc	ggc	gtg	gtg	gaa	tcc	gcc	att	gcc	gtt	912				
Ala	Arg	Leu	Asn	Met	Glu	Phe	Gly	Val	Val	Glu	Ser	Ala	Ile	Ala	Val					
290										295					300					
ggg	gga	cag	cag	ctc	acc	ctg	aag	ggg	ttg	ggc	ggc	gaa	tac	acc	gac	960				
Gly	Gly	Gln	Gln	Leu	Thr	Leu	Lys	Gly	Leu	Gly	Gly	Glu	Tyr	Thr	Asp					
305										310					315					320
atc	ttc	ctc	cca	ctg	tct	ggc	gcg	cac	caa	gca	gat	aat	gcc	gcg	gtt					
1008																				
Ile	Phe	Leu	Pro	Leu	Ser	Gly	Ala	His	Gln	Ala	Asp	Asn	Ala	Ala	Val					



325	330	335
gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca		
1056		
Ala Leu Ala	Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro	
340	345	350
ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca		
1104		
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro		
355	360	365
ggg cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca		
1152		
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala		
370	375	380
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt		
1200		
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg		
385	390	395
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac		
1248		
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp		
405	410	415
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa		
1296		
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu		
420	425	430
att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat		
1344		
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp		
435	440	445
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc		
1392		
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val		
450	455	460
caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa		
1440		
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu		
465	470	475
gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc		
1488		
Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile		
485	490	495
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca		
1533		
Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala		
500	505	510
tgagcaagcg tgaagaatca att		
1556		

&lt;210&gt; 698

&lt;211&gt; 511

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 698

Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn  
 1 5 10 15  
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser  
 20 25 30  
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu  
 35 40 45  
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu  
 50 55 60  
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met  
 65 70 75 80  
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala  
 85 90 95  
 Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile  
 100 105 110  
 Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser  
 115 120 125  
 Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro  
 130 135 140  
 Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr  
 145 150 155 160  
 Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met  
 165 170 175  
 Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp  
 180 185 190  
 Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp  
 195 200 205  
 Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val  
 210 215 220  
 Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala  
 225 230 235 240  
 Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly  
 245 250 255  
 Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu  
 260 265 270  
 Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val  
 275 280 285  
 Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val

290					295					300					
Gly 305	Gly	Gln	Gln	Leu	Thr 310	Leu	Lys	Gly	Leu	Gly 315	Gly	Glu	Tyr	Thr	Asp 320
Ile	Phe	Leu	Pro	Leu 325	Ser	Gly	Ala	His	Gln 330	Ala	Asp	Asn	Ala	Ala 335	Val
Ala	Leu	Ala	Ala 340	Val	Glu	Ala	Phe	Phe 345	Gly	Ala	Ser	Ala	Gly 350	Arg	Pro
Leu	Asp	Ile 355	Asp	Thr	Val	Arg	Glu 360	Gly	Phe	Ala	Gln	Val 365	Gln	Ser	Pro
Gly	Arg 370	Leu	Glu	Arg	Leu	Arg 375	Ser	Ala	Pro	Thr	Val 380	Phe	Ile	Asp	Ala
Ala 385	His	Asn	Pro	His	Gly 390	Ala	Ala	Ala	Leu	Gly 395	Ala	Ala	Leu	Asp	Arg 400
Asp	Phe	Glu	Phe	Arg 405	Arg	Leu	Ile	Gly	Val 410	Ile	Gly	Val	Leu	Cys 415	Asp
Lys	Asp	Ala	Arg 420	Gly	Ile	Leu	Glu	Ser 425	Leu	Glu	Pro	Tyr	Leu 430	His	Glu
Ile	Val	Cys 435	Thr	Gln	Thr	Ala	Ser 440	Glu	Arg	Ala	Leu	Asp 445	Ala	Tyr	Asp
Leu	Ala 450	Glu	Tyr	Ala	Arg	Glu 455	Ile	Tyr	Gly	Asp	Glu 460	Arg	Val	His	Val
Gln 465	Glu	Asp	Leu	Ala	Gly 470	Ala	Val	Glu	Leu	Ala 475	Ile	Glu	Leu	Ala	Glu 480
Asp	Thr	Asp	Val	Gln 485	Ser	Gly	Ser	Gly	Val 490	Val	Ile	Thr	Gly	Ser 495	Ile
Val	Thr	Ala	Gly 500	Asp	Ala	Arg	Thr	Leu 505	Phe	Gly	Lys	Glu	Pro	Ala 510	

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<210> 699
<211> 600
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(577)  
<223> RXA01517
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<400> 699
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gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg 115
Met His Ala Val Leu
1 5

tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg 163
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val

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	10	15	20	
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca				211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser				
	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val				
	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly				
	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly				
	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu				
	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala				
	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp				
	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp				
	135	140	145	
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat				597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile				
	150	155		
gca				600

&lt;210&gt; 700

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 700

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala				
1	5	10	15	

Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln				
20	25	30		

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu				
35	40	45		

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu				
50	55	60		

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg				
65	70	75	80	

<400> 701																	
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gtgcttttct	cgttgttttg	tggttttgtc	agaggatgtc	atg	cgc	ggt	tta	att									115
				Met	Arg	Val	Leu	Ile									
				1				5									
att	gat	aat	tat	gat	tct	ttc	acg	ttt	aat	ctc	gcc	acc	tat	gtg	gaa		163
Ile	Asp	Asn	Tyr	Asp	Ser	Phe	Thr	Phe	Asn	Leu	Ala	Thr	Tyr	Val	Glu		
				10				15						20			
gag	ggt	acg	ggt	cag	gca	cct	gtg	gtg	gtg	cct	aat	gat	caa	gaa	ata		211
Glu	Val	Thr	Gly	Gln	Ala	Pro	Val	Val	Val	Pro	Asn	Asp	Gln	Glu	Ile		
			25				30						35				
gat	gag	atg	ctt	ttc	gac	gcc	gtc	atc	ctc	tca	cct	ggc	ccg	ggc	cac		259
Asp	Glu	Met	Leu	Phe	Asp	Ala	Val	Ile	Leu	Ser	Pro	Gly	Pro	Gly	His		
		40					45					50					
gcc	ggc	ggt	gcg	gct	gat	ttt	ggt	atc	tgt	gca	ggc	gtc	att	gag	cgt		307
Ala	Gly	Val	Ala	Ala	Asp	Phe	Gly	Ile	Cys	Ala	Gly	Val	Ile	Glu	Arg		
		55				60					65						
gca	cgc	ggt	ccg	att	ttg	ggt	gtg	tgt	tta	ggc	cac	cag	ggc	att	gcg		355
Ala	Arg	Val	Pro	Ile	Leu	Gly	Val	Cys	Leu	Gly	His	Gln	Gly	Ile	Ala		
	70				75				80						85		
ttg	gcc	tat	ggc	ggt	gat	ggt	gat	ttg	gcg	ccc	agg	ccg	gtc	cac	ggt		403
Leu	Ala	Tyr	Gly	Gly	Asp	Val	Asp	Leu	Ala	Pro	Arg	Pro	Val	His	Gly		
			90					95						100			
gag	ggt	tcg	cag	atc	acc	cat	gat	ggt	tca	ggt	tta	ttt	gca	ggc	atc		451
Glu	Val	Ser	Gln	Ile	Thr	His	Asp	Gly	Ser	Gly	Leu	Phe	Ala	Gly	Ile		
			105				110						115				

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499  
 Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg  
 120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547  
 Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile  
 135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595  
 Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His  
 150 155 160 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643  
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe  
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691  
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile  
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739  
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His  
 200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787  
 Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu  
 215 220 225

ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc 835  
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly  
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883  
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser  
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931  
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly  
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979  
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser  
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa  
 1027  
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu  
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt  
 1075  
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe  
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct  
 1123  
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro  
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat  
 1171  
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr  
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg  
 1219  
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser  
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc  
 1267  
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala  
 375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat  
 1315  
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr  
 390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg  
 1363  
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro  
 410 415 420

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc  
 1411  
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro  
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa  
 1459  
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu  
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg  
 1507  
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu  
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc  
 1555  
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro  
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca  
 1603  
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr  
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt  
 1651  
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser  
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt  
 1699  
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly  
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct  
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala  
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc  
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly  
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat  
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn  
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt  
1983

Leu Phe Gly Val Glu Phe Pro  
615 620

<210> 702

<211> 620

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 702

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu  
1 5 10 15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro  
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
115 120 125



Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
 130 135 140  
 Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
 145 150 155 160  
 Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
 165 170 175  
 Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
 180 185 190  
 Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
 195 200 205  
 Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln  
 210 215 220  
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys  
 225 230 235 240  
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp  
 245 250 255  
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp  
 260 265 270  
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala  
 275 280 285  
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg  
 290 295 300  
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu  
 305 310 315 320  
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val  
 325 330 335  
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
 340 345 350  
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
 370 375 380  
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala  
 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
 420 425 430  
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
 435 440 445  
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

450	455	460
Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala		
465	470	475 480
Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val		
	485	490 495
Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu		
	500	505 510
Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly		
	515	520 525
Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp		
	530	535 540
Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr		
	545	550 555 560
Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu		
	565	570 575
Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu		
	580	585 590
Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser		
	595	600 605
Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro		
	610	615 620

&lt;210&gt; 703

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(724)

&lt;223&gt; RXA00958

&lt;400&gt; 703

attctaattcc tcaatctgaa gccgatgaga cgttgcacaa ggcgtatgcc gtgttgaatg 60

ccattgcgct tgctgctggt tccacttttg aggtcatccg	atg aca cac gtt gtt	115
	Met Thr His Val Val	
	1 5	

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc	163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe	
	10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg	211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val	
	25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga	259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly	
	40 45 50

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cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
    55                60                65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
    70                75                80                85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
                90                95                100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
                105                110                115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
    120                125                130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
    135                140                145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
    150                155                160                165

ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
                170                175                180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
                185                190                195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
    200                205

tca 747

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&lt;210&gt; 704

&lt;211&gt; 208

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 704

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Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
  1                5                10                15

Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
    20                25                30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
    35                40                45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
    50                55                60

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Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His  
 130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr  
 145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp  
 165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro  
 180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 195 200 205

<210> 705  
 <211> 1266  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1243)  
 <223> RXA02790

<400> 705  
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agggaaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115  
 Met Glu Pro Val Tyr  
 1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163  
 Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
 10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211  
 Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
 25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259  
 Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val  
 40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa	307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu	
55 60 65	
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc	355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser	
70 75 80 85	
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	
90 95 100	
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac	451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	
105 110 115	
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac	499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	
120 125 130	
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	
135 140 145	
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag	595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu	
150 155 160 165	
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc	643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	
170 175 180	
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag	691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys	
185 190 195	
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc	739
Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	
200 205 210	
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac	787
Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	
215 220 225	
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	835
His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	
230 235 240 245	
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	883
Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala	
250 255 260	
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc	931
Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	
265 270 275	
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	979
Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	
280 285 290	

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc  
1027

Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr  
295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc  
1075

Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala  
310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga  
1123

Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly  
330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc  
1171

Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe  
345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac  
1219

Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn  
360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaaat tgg  
1266

Ser Gly Val Leu Asp Ser Asn Arg  
375 380

<210> 706

<211> 381

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 706

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr  
1 5 10 15

Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val  
20 25 30

Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly  
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu  
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe  
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly  
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala  
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly  
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly  
 130 135 140  
 Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn  
 145 150 155 160  
 Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro  
 165 170 175  
 Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg  
 180 185 190  
 Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr  
 195 200 205  
 Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile  
 210 215 220  
 Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala  
 225 230 235 240  
 Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu  
 245 250 255  
 Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val  
 260 265 270  
 Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr  
 275 280 285  
 Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp  
 290 295 300  
 Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro  
 305 310 315 320  
 Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu  
 325 330 335  
 Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350  
 Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
 355 360 365  
 Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
 370 375 380

&lt;210&gt; 707

&lt;211&gt; 579

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(556)

&lt;223&gt; RXA00106

&lt;400&gt; 707

tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg 60

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gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
Met Ile Gly Ala Ile
1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

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&lt;210&gt; 708

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 708

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Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
1 5 10 15

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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
20 25 30

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Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
35 40 45

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Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser  
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Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
 65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
 85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
 100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
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Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr  
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Lys Phe Gln Arg Tyr Ile Lys Val  
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<210> 709  
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<220>  
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 <223> RXN02198

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 Met Ser Thr Ser Val  
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
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ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu  
 25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259  
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly  
 40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307  
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
 55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355  
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr  
 70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403  
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

	90								95				100						
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	cys arg glu leu ala tyr lys gly thr ala val ala arg glu val ala	451																	
	105	110	115																
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	asp glu met gly pro gly arg asn gly met arg arg phe val val gly	499																	
	120	125	130																
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat	ser leu gly pro gly thr lys leu pro ser leu gly his ala pro tyr	547																	
	135	140	145																
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac	ala asp leu arg gly his tyr lys glu ala ala leu gly ile ile asp	595																	
	150	155	160																
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag	gly gly gly asp ala phe leu ile glu thr ala gln asp leu leu gln	643																	
	170	175	180																
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat	val lys ala ala val his gly val gln asp ala met ala glu leu asp	691																	
	185	190	195																
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	thr phe leu pro ile ile cys his val thr val glu thr thr gly thr	739																	
	200	205	210																
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca	met leu met gly ser glu ile gly ala ala leu thr ala leu gln pro	787																	
	215	220	225																
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	leu gly ile asp met ile gly leu asn cys ala thr gly pro asp glu	835																	
	230	235	240																
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	met ser glu his leu arg tyr leu ser lys his ala asp ile pro val	883																	
	250	255	260																
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	ser val met pro asn ala gly leu pro val leu gly lys asn gly ala	931																	
	265	270	275																
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc	glu tyr pro leu glu ala glu asp leu ala gln ala leu ala gly phe	979																	
	280	285	290																
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca	val ser glu tyr gly leu ser met val gly gly cys cys gly thr thr	1027																	
	295	300	305																
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag	pro glu his ile arg ala val arg asp ala val val gly val pro glu	1075																	
	310	315	320	325															

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag  
1123

Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln  
330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc  
1171

Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr  
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc  
1219

Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg  
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc  
1267

Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly  
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt  
1315

Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly  
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc  
1363

Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr  
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg  
1411

Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu  
425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt  
1459

Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu  
440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac  
1507

Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp  
455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag  
1555

Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys  
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag  
1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac  
1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac  
1699  
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat  
1747  
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca  
1795  
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac  
1843  
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att  
1891  
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
1939  
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc  
1987  
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag  
2035  
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa  
2083  
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu  
650 655 660

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2131  
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
665 670 675

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2179  
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
680 685 690

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2227  
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac  
2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca  
2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg  
2563

Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
810 815 820

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2599

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<210> 710

<211> 833

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 710

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20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
 85 90 95  
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
 100 105 110  
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
 115 120 125  
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
 130 135 140  
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
 145 150 155 160  
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
 165 170 175  
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
 180 185 190  
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
 195 200 205  
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
 210 215 220  
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
 225 230 235 240  
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
 245 250 255  
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
 260 265 270  
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
 275 280 285  
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
 290 295 300  
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
 305 310 315 320  
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
 340 345 350  
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
 355 360 365  
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
 370 375 380  
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln  
 385 390 395 400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
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 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
 515 520 525  
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
 530 535 540  
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
 565 570 575  
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys  
 645 650 655  
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu  
 660 665 670  
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu  
 675 680 685  
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp  
 690 695 700  
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln  
 705 710 715 720  
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

725	730	735
Val Ala Tyr Leu Glu Pro Phe Met	Glu Glu Glu Ala Glu Ala Thr Gly	
740	745	750
Ser Ala Gln Ala Glu Gly Lys Gly Lys	Ile Val Val Ala Thr Val Lys	
755	760	765
Gly Asp Val His Asp Ile Gly Lys Asn	Leu Val Asp Ile Ile Leu Ser	
770	775	780
Asn Asn Gly Tyr Asp Val Val Asn	Leu Gly Ile Lys Gln Pro Leu Ser	
785	790	795
Ala Met Leu Glu Ala Ala Glu Glu His	Lys Ala Asp Val Ile Gly Met	
805	810	815
Ser Gly Leu Leu Val Lys Ser Thr	Val Val Met Lys Gln Thr Ile Ser	
820	825	830

Asp

&lt;210&gt; 711

&lt;211&gt; 2578

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2578)

&lt;223&gt; FRXA02198

&lt;400&gt; 711

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	Met Ser Thr Ser Val	
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act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg	163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala	
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ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc	211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu	
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caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg	259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly	
40 45 50	

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att	307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile	
55 60 65	

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His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr	
70 75 80 85	



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Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
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tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
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gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
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Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
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Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	
150 155 160 165	
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Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
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Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
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Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
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Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
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Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
280 285 290	
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Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
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Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
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 1171  
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 345 350 355

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 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg  
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc  
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 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly  
 375 380 385

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 455 460 465

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 490 495 500

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 505 510 515

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1699  
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520 525 530

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Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
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Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
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gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac  
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Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
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1891  
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
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1939  
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
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1987  
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615 620 625

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2083  
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650 655 660

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2131  
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
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2179  
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
680 685 690

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2227  
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
695 700 705

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2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
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2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
730 735 740

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2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
745 750 755

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2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

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2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
775 780 785

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2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
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Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
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Asp	Ile	Ala	Asp	Arg	Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val		
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Ala	Arg	Glu	Val	Ala	Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg		
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Arg	Phe	Val	Val	Gly	Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu		
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Gly	His	Ala	Pro	Tyr	Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala		
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Gln	Asp	Leu	Leu	Gln	Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala		
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Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val		
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 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
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 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
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 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
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 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
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 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
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 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
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 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
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 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
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 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp  
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 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

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Val Ala Tyr	Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly				
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Ser Ala Gln	Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys				
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Gly Asp Val	His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser				
	770		775		780
Asn Asn Gly	Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser				
	785		790		795
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Ser Gly Leu	Leu Val Lys Ser Thr Val Val				
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Met Thr Ser Asn Phe	
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Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	
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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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acc aag tgg ttt gat acc aac tac cac tac ctg gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
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gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
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gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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1123	



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Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala 710 715 720 725		

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2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
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2358

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35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
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Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
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Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
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Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
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Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
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145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
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Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
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Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
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Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val						
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Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu						
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Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala						
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Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro						
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Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg						
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Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr						
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Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala						
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Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met						
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Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu						
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Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln						
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Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr						
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Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr						
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 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
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 595 600 605  
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln  
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 Met Thr Ser Asn Phe  
 1 5  
  
 tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163  
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu  
 10 15 20  
  
 aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211  
 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

25	30	35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259		
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu			
40 45 50			
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307		
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala			
55 60 65			
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355		
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp			
70 75 80 85			
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403		
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg			
90 95 100			
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451		
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met			
105 110 115			
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499		
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser			
120 125 130			
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547		
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu			
135 140 145			
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595		
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly			
150 155 160 165			
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643		
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro			
170 175 180			
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691		
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys			
185 190 195			
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739		
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr			
200 205 210			
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787		
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr			
215 220 225			
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835		
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly			
230 235 240 245			
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883		
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly			
250 255 260			
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931		
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly			
265 270 275			

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
           280                          285                          290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
           295                          300                          305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
           310                          315                          320                          325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
                           330                          335                          340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
                           345                          350                          355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
                           360                          365                          370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
           375                          380                          385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
           390                          395                          400                          405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
                           410                          415                          420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
                           425                          430                          435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
           440                          445                          450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507  
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
           455                          460                          465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg  
1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr  
585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt  
1923

Arg Arg Arg  
600

<210> 716

<211> 600

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 716

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Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser  
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45



Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
 50 55 60  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 65 70 75 80  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
 85 90 95  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
 100 105 110  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
 115 120 125  
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
 130 135 140  
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
 145 150 155 160  
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
 165 170 175  
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
 180 185 190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
 195 200 205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala  
 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

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      370              375              380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
385              390              395              400

Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
              405              410              415

Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
              420              425              430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
              435              440              445

Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
              450              455              460

Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
465              470              475              480

Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
              485              490              495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
              500              505              510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
              515              520              525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
              530              535              540

Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
545              550              555              560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
              565              570              575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
              580              585              590

Leu Leu Pro Ala Thr Arg Arg Arg
              595              600

<210> 717
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> FRXA02086

<400> 717
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aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115
              Met Ser Leu Arg Phe
              1              5

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gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
      10      15      20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
      25      30      35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc* aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
      40      45      50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
      55      60      65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
      70      75      80      85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
      90      95      100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
      105      110      115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
      120      125      130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
      135      140      145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
      150      155      160

aac 603

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&lt;210&gt; 718

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 718

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Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
 1          5          10          15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
      20      25      30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35      40      45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
      50      55      60

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Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95  
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110  
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
 115 120 125  
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
 130 135 140  
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 145 150 155 160

<210> 719  
 <211> 1326  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1303)  
 <223> RXN02648

<400> 719  
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 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5  
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
 gat gca aac atc aag cgt tct tct gta gat gac gtg atc aag cgc cag gtt 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50  
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85  
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403

Leu Gly Gly	Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu	
	90 95 100	
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat	451	
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp		
	105 110 115	
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct	499	
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser		
	120 125 130	
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga	547	
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly		
	135 140 145	
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg	595	
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu		
	150 155 160 165	
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca	643	
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala		
	170 175 180	
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac	691	
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp		
	185 190 195	
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa	739	
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu		
	200 205 210	
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg	787	
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro		
	215 220 225	
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag	835	
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys		
	230 235 240 245	
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883	
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala		
	250 255 260	
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	931	
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly		
	265 270 275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979	
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile		
	280 285 290	
ggg gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca		
1027		
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala		
	295 300 305	
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt		
1075		
Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu		
	310 315 320 325	

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
390 395 400

aacgagggtt gct  
1326

<210> 720

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220  
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
 225 230 235 240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
 245 250 255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
 260 265 270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
 275 280 285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
 290 295 300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
 305 310 315 320  
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
 325 330 335  
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
 340 345 350  
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
 355 360 365  
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
 370 375 380  
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
 385 390 395 400

Phe

&lt;210&gt; 721

&lt;211&gt; 548

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(525)

&lt;223&gt; FRXA02648

&lt;400&gt; 721

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gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1           5           10           15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20           25           30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35           40           45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
          50           55           60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
          65           70           75           80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
          85           90           95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
          100          105          110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
          115          120          125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
          130          135          140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
          145          150          155          160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          165          170          175

taagctagac aacgagggtt gct 548

```

&lt;210&gt; 722

&lt;211&gt; 175

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 722

```

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1           5           10           15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20           25           30

```



Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
           35                                  40                                  45  
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
           50                                  55                                  60  
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
           65                                  70                                  75                                  80  
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
                                   85                                  90                                  95  
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
                                   100                                  105                                  110  
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
           115                                  120                                  125  
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
           130                                  135                                  140  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
           145                                  150                                  155                                  160  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
                                   165                                  170                                  175

&lt;210&gt; 723

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(784)

&lt;223&gt; FRXA02658

&lt;400&gt; 723

atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcggttag agtcgaatga 60

gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
   Met Ser Gln Asn Arg  
   1                                  5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
                                   10                                  15                                  20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
                                   25                                  30                                  35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
                                   40                                  45                                  50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
                                   55                                  60                                  65

```

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
215 220 225

```

&lt;210&gt; 724

&lt;211&gt; 228

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 724

```

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn

```



Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Pro Gly Arg  
 130 135 140  
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480  
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160  
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528  
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175  
 taacaccttt gagaggaaa act 551

&lt;210&gt; 726

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 726

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe  
 1 5 10 15  
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30  
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45  
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg

130																				
Ile	Gly	Val	Glu	Leu	Ser	Glu	Glu	Leu	Gln	Leu	His	Pro	Glu	Gln	Ser					
145					150					155					160					
Thr	Asp	Ala	Phe	Val	Leu	Tyr	His	Pro	Glu	Ala	Lys	Tyr	Phe	Asn	Val					
				165					170					175						
<p>&lt;210&gt; 727</p> <p>&lt;211&gt; 546</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; <i>Corynebacterium glutamicum</i></p> <p>&lt;220&gt;</p> <p>&lt;221&gt; CDS</p> <p>&lt;222&gt; (101)..(523)</p> <p>&lt;223&gt; RXC00988</p> <p>&lt;400&gt; 727</p>																				
tagcagaaga caccgatgta cagtcgcat caggtgttgt gatcaccggt tcaatcgtga 60																				
ccgccggcga tgcgcgcacg ctgtttggaa aggaacctgc															atg agc aag cgt gaa					115
															Met Ser Lys Arg Glu					
															1 5					
gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag															163					
Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys																				
															10 15 20					
gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg															211					
Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met																				
															25 30 35					
gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac															259					
Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp																				
															40 45 50					
gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc															307					
Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val																				
															55 60 65					
gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc															355					
Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser																				
															70 75 80 85					
atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt															403					
Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe																				
															90 95 100					
gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg															451					
Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp																				
															105 110 115					
gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc															499					
Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg																				
															120 125 130					

ggg ctg ctt acc acg cag cac agc taagctttaa ggcctccgg ggc 546  
 Gly Leu Leu Thr Thr Gln His Ser  
 135 140

<210> 728

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<400> 728

Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly  
 1 5 10 15

His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala  
 20 25 30

Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val  
 35 40 45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val  
 50 55 60

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln  
 65 70 75 80

Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala  
 85 90 95

Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile  
 100 105 110

Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile  
 115 120 125

Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser  
 130 135 140

<210> 729

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXC01518

<400> 729

agcagaacct gatgccgtcc tgcacggcac gaccattgca gaacatgtgg ataatttga 60

tcccacagac attgaaggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115  
 Val Ala Phe Met Gln  
 1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163  
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala  
 10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile  
                   25                                  30                                  35  
 tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259  
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly  
                   40                                  45                                  50  
 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307  
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly  
                   55                                  60                                  65  
 cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355  
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met  
                   70                                  75                                  80                                  85  
 ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403  
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr  
                                   90                                  95                                  100  
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451  
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala  
                                   105                                  110                                  115  
 gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499  
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile  
                   120                                  125                                  130  
 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547  
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro  
                   135                                  140                                  145  
 cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcattgaatc 594  
 Pro Pro Gln Ser Gly Glu Ala Ile Ser  
                   150                                  155  
 aag 597

&lt;210&gt; 730

&lt;211&gt; 158

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 730

Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly  
   1                                  5                                  10                                  15  
 Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly  
                   20                                  25                                  30  
 Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu  
                   35                                  40                                  45  
 Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp  
                   50                                  55                                  60  
 Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile  
                   65                                  70                                  75                                  80  
 Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile  
                   85                                  90                                  95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala  
 100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys  
 115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg  
 130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser  
 145 150 155

<210> 731  
 <211> 723  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(700)  
 <223> RXC01942

<400> 731  
 gccgcgaaat tcggtgaaat tgaaggtatt cctgcagatc aggcaaattc ttccacgact 60

gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115  
 Met Leu Arg Ile Gly  
 1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163  
 Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu  
 10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211  
 Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp  
 25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259  
 Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe  
 40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307  
 Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu  
 55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355  
 Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala  
 70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403  
 Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu  
 90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451  
 Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu  
 105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499  
 Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp



120	125	130	
gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc			547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu			
135	140	145	
aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac			595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp			
150	155	160	165
gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta			643
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu			
	170	175	180
gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt			691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser			
	185	190	195
cgc gtg aat tagcactaaa acatcgtcaa agt			723
Arg Val Asn			
200			
<210> 732			
<211> 200			
<212> PRT			
<213> <i>Corynebacterium glutamicum</i>			
<400> 732			
Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr			
1	5	10	15
Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp			
	20	25	30
Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu			
	35	40	45
Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu			
	50	55	60
Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr			
	65	70	75
Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala			
	85	90	95
Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr			
	100	105	110
Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu			
	115	120	125
Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val			
	130	135	140
Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser			
	145	150	155
Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp			
	165	170	175

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile  
 180 185 190

Ala Glu Ile Leu Ser Arg Val Asn  
 195 200

<210> 733

<211> 1194

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1171)

<223> RXN02802

<400> 733

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agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115  
 Val Lys Asn Leu Asp  
 1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163  
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln  
 10 15 20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211  
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly  
 25 30 35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259  
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly  
 40 45 50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307  
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His  
 55 60 65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355  
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu  
 70 75 80 85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403  
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr  
 90 95 100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451  
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala  
 105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499  
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His  
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca 547  
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala  
 135 140 145

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tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac 595
Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His
150 155 160 165

ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc 643
Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Pro Gly Ser
170 175 180

gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta 691
Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val
185 190 195

atg ggc tcc gcg atg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg 739
Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val
200 205 210

ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc 787
Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly
215 220 225

acc tgg gaa tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg 835
Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg
230 235 240 245

gtg ctt ggg tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag 883
Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu
250 255 260

gtg ctc gat gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc 931
Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu
265 270 275

atc gac gtc cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc 979
Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly
280 285 290

gcg cac aac acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc
1027
Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro
295 300 305

tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc
1075
Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val
310 315 320 325

cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga
1123
Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly
330 335 340

atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg
1171
Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
345 350 355

taaaaccaag gcgttggtgcc acc
1194

```

&lt;210&gt; 734

&lt;211&gt; 357

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 734

```

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
  1             5             10             15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
          20             25             30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
      35             40             45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
  50             55             60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
  65             70             75             80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
          85             90             95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
      100             105             110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
      115             120             125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
      130             135             140

Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val
      145             150             155             160

Phe His Ala Gly His Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro
          165             170             175

Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly
      180             185             190

Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys
      195             200             205

Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr
      210             215             220

Ser Ser Leu Asp Gly Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro
      225             230             235             240

Glu Val Leu Glu Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser
          245             250             255

Gly Gly Phe Gly Glu Val Leu Asp Val Pro Arg Val Ser Ala Leu Val
      260             265             270

Asp Gly Val Ser Leu Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala
      275             280             285

Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu
      290             295             300

```

Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr  
 305 310 315 320  
 Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser  
 325 330 335  
 Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp  
 340 345 350  
 Leu Asp Ser Leu Gly  
 355

&lt;210&gt; 735

&lt;211&gt; 497

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(474)

&lt;223&gt; FRXA02802

&lt;400&gt; 735

tccgcgatg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg ggc aca ccc 51  
 Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro  
 1 5 10 15  
 ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa 99  
 Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu  
 20 25 30  
 tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg gtg ctt ggg 147  
 Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly  
 35 40 45  
 tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag gtg ctc gat 195  
 Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp  
 50 55 60  
 gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc atc gac gtc 243  
 Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val  
 65 70 75  
 cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac 291  
 Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn  
 80 85 90 95  
 acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc 339  
 Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser  
 100 105 110  
 gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca 387  
 Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala  
 115 120 125  
 caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc 435  
 Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser  
 130 135 140

ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaaccaag 484  
 Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly  
 145 150 155

gcgttggtgcc acc 497

<210> 736

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 736

Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro Leu  
 1 5 10 15

Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu Tyr  
 20 25 30

Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly Ser  
 35 40 45

Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp Val  
 50 55 60

Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg  
 65 70 75 80

Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn Thr  
 85 90 95

Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser Ala  
 100 105 110

Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala Gln  
 115 120 125

Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser Leu  
 130 135 140

Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly  
 145 150 155

<210> 737

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA00438

<400> 737

ccttcgccgc ctgctccgac ctcgccgacg ccgtcaaagc ccaggtcccg atctggaaag 60

agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115  
 Val Lys Asn Leu Asp  
 1 5

```

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
      10                      15                      20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
      25                      30                      35

ggc ctc ggc tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
      40                      45                      50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
      55                      60                      65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
      70                      75                      80                      85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
      90                      95                      100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
      105                      110                      115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
      120                      125                      130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro
      135                      140                      145

```

&lt;210&gt; 738

&lt;211&gt; 145

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 738

```

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
  1                      5                      10                      15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
      20                      25                      30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
      35                      40                      45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
      50                      55                      60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
      65                      70                      75                      80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
      85                      90                      95

```

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala  
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn  
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile  
 130 135 140

Pro  
 145

<210> 739  
 <211> 579  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(556)  
 <223> RXN00437

<400> 739  
 ttcatcatgg cgctgcccg ctccacgggt gcggcgcgcg atgccaccgc tgtcctcgac 60

ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115  
 Met Asn Thr Asp Pro  
 1 5

gct tac gtc gcc gaa caa acc ggc aaa ctc atc gac gct ttc ctc acc 163  
 Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile Asp Ala Phe Leu Thr  
 10 15 20

acc gac ccc ctc gaa ccg ctg ctc gac gcc gcc aaa aac ggc gtc tgc 211  
 Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala Lys Asn Gly Val Cys  
 25 30 35

aca gag gcg atg ggc gcg ctg gtc acc ttc gaa ggc atc gtc cgc gac 259  
 Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu Gly Ile Val Arg Asp  
 40 45 50

cac gac ggc ggc gcc cgc gtg acc tcc ctg acc tac acc gcg cat ccc 307  
 His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr Tyr Thr Ala His Pro  
 55 60 65

acc gcg ccg cag gtc ctt tct gct gtc gcg gac tcc atc gtt gaa aaa 355  
 Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp Ser Ile Val Glu Lys  
 70 75 80 85

cac ccg cgc acc cgc ctc tgg acc gcg cac cgc acc ggc gcc ttg aaa 403  
 His Pro Arg Thr Arg Leu Trp Thr Ala His Arg Thr Gly Ala Leu Lys  
 90 95 100

atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc tcc gcc cac cgc gcc 451  
 Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala Ser Ala His Arg Ala  
 105 110 115

gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac gcc gtc aaa gcc cag 499  
 Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp Ala Val Lys Ala Gln  
 120 125 130



gtc ccg atc tgg aaa gag caa acg cgc ctc gac ggc tcc acc gat tgg 547  
 Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp Gly Ser Thr Asp Trp  
           135                          140                          145

gtc ggc ctg tgaaaaacct cgacatcgcc cgc 579  
 Val Gly Leu  
 150

<210> 740

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 740

Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile  
           1                          5                          10                          15

Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala  
                           20                          25                          30

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu  
                           35                          40                          45

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr  
           50                          55                          60

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp  
           65                          70                          75                          80

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg  
                           85                          90                          95

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala  
                           100                          105                          110

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp  
           115                          120                          125

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp  
           130                          135                          140

Gly Ser Thr Asp Trp Val Gly Leu  
 145                          150

<210> 741

<211> 383

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (360)

<223> FRXA00437

<400> 741

aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48  
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu  
           1                          5                          10                          15

```

ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20              25              30

tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35              40              45

tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50              55              60

acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65              70              75              80

tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85              90              95

gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100             105             110

ggc tcc acc gat tgg gtc ggc ctg tgaaaaacct cgacatcgcc cgc 383
Gly Ser Thr Asp Trp Val Gly Leu
      115             120

```

&lt;210&gt; 742

&lt;211&gt; 120

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 742

```

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
  1              5              10              15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20              25              30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35              40              45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50              55              60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65              70              75              80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85              90              95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100             105             110

Gly Ser Thr Asp Trp Val Gly Leu
      115             120

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<210> 743
<211> 591
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(568)
<223> RXN00439
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<400> 743																	
ctgccaccgc agactgtctg atcaggatcc cggcgcgggac tacggtggag gaaaacgaca																	60
tcgttaagat ttacccattc aactaacagg agttaattta atg agc gag ctc acc																	115
Met Ser Glu Leu Thr																	5
cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa																	163
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys																	20
aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg																	211
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg																	35
ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac																	259
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp																	40
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg																	307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr																	55
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act																	355
Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr																	70
gtg gat ttt ttt gag ctt act gat ggt gtt cgg att gag gct tcg gtg																	403
Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val																	90
aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg																	451
Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val																	105
agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag																	499
Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys																	120
atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa																	547
Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys																	135
tct ggg gat tgg tct gtt cag tgacagctct ggttatcggt gcg																	591
Ser Gly Asp Trp Ser Val Gln																	150

<210>	744
<211>	156
<212>	PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 744

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val  
 1 5 10 15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly  
 20 25 30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly  
 35 40 45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met  
 50 55 60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro  
 65 70 75 80

Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg  
 85 90 95

Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu  
 100 105 110

Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile  
 115 120 125

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser  
 130 135 140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln  
 145 150 155

&lt;210&gt; 745

&lt;211&gt; 218

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(195)

&lt;223&gt; FRXA00439

&lt;400&gt; 745

act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act 48  
 Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr  
 1 5 10 15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg 96  
 Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr  
 20 25 30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc 144  
 Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly  
 35 40 45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt 192  
 Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val  
 50 55 60

cag tgacagctct gggtatcggt gcg

218

Gln

65

&lt;210&gt; 746

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 746

Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr  
 1 5 10 15

Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr  
 20 25 30

Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly  
 35 40 45

Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val  
 50 55 60

Gln

65

&lt;210&gt; 747

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(358)

&lt;223&gt; FRXA00442

&lt;400&gt; 747

ctgccaccgc agactgtctg atcaggatcc cggcgccggac tacggtggag gaaaacgaca 60

tcgttaagat ttaccattc aactaacagg agttaattta atg agc gag ctc acc 115  
 Met Ser Glu Leu Thr  
 1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163  
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys  
 10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211  
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg  
 25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259  
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp  
 40 45 50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307  
 Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr  
 55 60 65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355

Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr  
 70 75 80 85

gtg 358  
 Val

<210> 748  
 <211> 86  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 748  
 Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val  
 1 5 10 15  
 Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly  
 20 25 30  
 Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly  
 35 40 45  
 Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met  
 50 55 60  
 Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro  
 65 70 75 80  
 Leu Gly Lys Ile Thr Val  
 85

<210> 749  
 <211> 582  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(559)  
 <223> RXA00440

<400> 749  
 cggatatacga catgatcaag gctgtggata agatggccgt gattgatggc attcgtgtgc 60  
 tgtcgaaaac tggcggtaaa tctggggatt ggtctgttca gtg aca gct ctg gtt 115  
 Val Thr Ala Leu Val  
 1 5  
 atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163  
 Ile Val Ala Ser Thr Arg Ala Ala Gly Val Tyr Glu Asp Arg Ser  
 10 15 20  
 ggc cca att ttg gtg tcg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211  
 Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro  
 25 30 35  
 gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259  
 Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu  
 40 45 50

ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307  
 Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr  
 55 60 65  
 cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355  
 Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu  
 70 75 80 85  
 atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403  
 Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val  
 90 95 100  
 ccg acc gca gta ttg tcg cgc acc gtc gcg ggc acc atc ggc ggc agt 451  
 Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser  
 105 110 115  
 ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499  
 Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr  
 120 125 130  
 gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547  
 Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly  
 135 140 145  
 cac cat gaa cac tgaccccgct tacgtcgccg aac 582  
 His His Glu His  
 150

&lt;210&gt; 750

&lt;211&gt; 153

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val  
 1 5 10 15  
 Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys  
 20 25 30  
 Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro  
 35 40 45  
 Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly  
 50 55 60  
 Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro  
 65 70 75 80  
 Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr  
 85 90 95  
 Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly  
 100 105 110  
 Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala  
 115 120 125  
 Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr

130 135 140

Gly Thr Leu Gln Gly His His Glu His  
145 150

<210> 751  
<211> 1287  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1264)  
<223> RXN00441

<400> 751  
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agcgttacga ttgttttcca aggtgagaaa ggtttaattg atg tct cgt tcg ccg 115  
Met Ser Arg Ser Pro  
1 5

gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163  
Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser  
10 15 20

acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg 211  
Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala  
25 30 35

gtc act gcg cag tgg gat tcg cca cgt ttt gat aat tcc caa atg gat 259  
Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp  
40 45 50

ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc 307  
Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val  
55 60 65

ggc cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga 355  
Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg  
70 75 80 85

ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct 403  
Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro  
90 95 100

aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat 451  
Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn  
105 110 115

ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc 499  
Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe  
120 125 130

ata cgg ttg cag ggt tcg gat att act gcc ggc gac gag atc att cca 547  
Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro  
135 140 145

gca ggt acg gag ctt aac tcg gtg cac atc ggg gtg ttg gct agt cag 595  
Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln



150	155	160	165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc	643			
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile				
170 175 180				
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct	691			
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro				
185 190 195				
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc	739			
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile				
200 205 210				
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc	787			
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg				
215 220 225				
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc	835			
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile				
230 235 240 245				
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc	883			
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile				
250 255 260				
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct	931			
Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro				
265 270 275				
ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca	979			
Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser				
280 285 290				
ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc				
1027				
Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val				
295 300 305				
gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc				
1075				
Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile				
310 315 320 325				
acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc				
1123				
Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg				
330 335 340				
ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct				
1171				
Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro				
345 350 355				
ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct				
1219				
Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser				
360 365 370				
gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt				
1264				

Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg  
 375 380 385

taagatttac ccattcaact aac  
 1287

<210> 752

<211> 388

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 752

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Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg  
 20 25 30

Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp  
 35 40 45

Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly  
 50 55 60

Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp  
 65 70 75 80

Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr  
 85 90 95

Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys  
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr  
 115 120 125

Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly  
 130 135 140

Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly  
 145 150 155 160

Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro  
 165 170 175

Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly  
 180 185 190

Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys  
 195 200 205

Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp  
 210 215 220

Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln  
 225 230 235 240

Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu  
 245 250 255

Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His  
 260 265 270

Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu  
 275 280 285

Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser  
 290 295 300

Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His  
 305 310 315 320

Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg  
 325 330 335

Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro  
 340 345 350

Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys  
 355 360 365

His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly  
 370 375 380

Lys Arg His Arg  
 385

&lt;210&gt; 753

&lt;211&gt; 815

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(792)

&lt;223&gt; FRXA00441

&lt;400&gt; 753

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Ile	Pro	Ala	Thr	Pro	Gln	Gly	Gln	Phe	Ile	Arg	Leu	Gln	Gly	Ser	Asp	
1				5				10					15			
att	act	gcc	ggc	gac	gag	atc	att	cca	gca	ggt	acg	gag	ctt	aac	tcg	96
Ile	Thr	Ala	Gly	Asp	Glu	Ile	Ile	Pro	Ala	Gly	Thr	Glu	Leu	Asn	Ser	
			20					25					30			
gtg	cac	atc	ggg	gtg	ttg	gct	agt	cag	tcg	atc	aag	agc	att	gaa	gtc	144
Val	His	Ile	Gly	Val	Leu	Ala	Ser	Gln	Ser	Ile	Lys	Ser	Ile	Glu	Val	
			35				40					45				
gca	gca	aag	cca	cgt	gtc	ctc	atc	atc	acc	ggc	ggg	tct	gaa	att	tca	192
Ala	Ala	Lys	Pro	Arg	Val	Leu	Ile	Ile	Thr	Gly	Gly	Ser	Glu	Ile	Ser	
			50				55				60					
gaa	cag	cac	gga	ccc	gcc	acg	atc	cct	gat	gcc	aac	ggc	cct	ctg	ctt	240
Glu	Gln	His	Gly	Pro	Ala	Thr	Ile	Pro	Asp	Ala	Asn	Gly	Pro	Leu	Leu	
65					70					75				80		
cgt	tcc	ctg	tgc	gcc	cgc	aac	aat	atc	gag	gtc	atc	gcg	gga	ctg	cac	288
Arg	Ser	Leu	Cys	Ala	Arg	Asn	Asn	Ile	Glu	Val	Ile	Ala	Gly	Leu	His	

85										90					95					
acc aac gac gat cct gaa cga ctc cgc ttt gaa ctg gaa aac gcc att	336																			
Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile																				
100 105 110																				
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac	384																			
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His																				
115 120 125																				
ggg aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc	432																			
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser																				
130 135 140																				
tgg ttt gga cat gtc gat cag cag cct ggc ggt cct caa ggc atc tcc	480																			
Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser																				
145 150 155 160																				
act ttt gct gaa act cct gtc att tca ctt ccc gga aat ccg att tcc	528																			
Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser																				
165 170 175																				
acc ttg gtg agt ttc aca ctt ttg gtc gcg cca gcg ctc aac cgc cag	576																			
Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln																				
180 185 190																				
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg	624																			
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu																				
195 200 205																				
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac	672																			
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn																				
210 215 220																				
ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct	720																			
Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala																				
225 230 235 240																				
ggg tca agc tgc cac cgc aga ctg tct gat cag gat ccc ggc gcg gac	768																			
Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp																				
245 250 255																				
tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac	815																			
Tyr Gly Gly Gly Lys Arg His Arg																				
260																				

&lt;210&gt; 754

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 754

Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp
1 5 10 15

Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
20 25 30

Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
35 40 45

Ala	Ala	Lys	Pro	Arg	Val	Leu	Ile	Ile	Thr	Gly	Gly	Ser	Glu	Ile	Ser		
50						55						60					
Glu	Gln	His	Gly	Pro	Ala	Thr	Ile	Pro	Asp	Ala	Asn	Gly	Pro	Leu	Leu		
65					70					75					80		
Arg	Ser	Leu	Cys	Ala	Arg	Asn	Asn	Ile	Glu	Val	Ile	Ala	Gly	Leu	His		
				85					90					95			
Thr	Asn	Asp	Asp	Pro	Glu	Arg	Leu	Arg	Phe	Glu	Leu	Glu	Asn	Ala	Ile		
			100					105					110				
Asp	Gln	Tyr	Gln	Pro	Asp	Val	Ile	Ile	Thr	Ser	Gly	Gly	Ile	Ser	His		
		115					120					125					
Gly	Lys	Phe	Glu	Val	Phe	Arg	Gln	Ile	Leu	Glu	Gly	Thr	Pro	Asn	Ser		
	130					135					140						
Trp	Phe	Gly	His	Val	Asp	Gln	Gln	Pro	Gly	Gly	Pro	Gln	Gly	Ile	Ser		
145					150					155					160		
Thr	Phe	Ala	Glu	Thr	Pro	Val	Ile	Ser	Leu	Pro	Gly	Asn	Pro	Ile	Ser		
				165					170					175			
Thr	Leu	Val	Ser	Phe	Thr	Leu	Leu	Val	Ala	Pro	Ala	Leu	Asn	Arg	Gln		
			180					185					190				
Pro	Leu	Arg	His	Leu	Asp	Ala	Arg	Ile	Thr	Ala	Pro	Val	Gln	Gly	Leu		
		195					200					205					
Gln	Asp	Asn	Arg	Glu	Gln	Phe	Leu	Arg	Gly	Thr	Ile	Ser	Tyr	Arg	Asn		
	210					215					220						
Gly	Pro	Arg	Pro	Arg	His	Ala	Ser	Pro	Gly	His	Gln	Phe	Pro	Pro	Ala		
225					230					235					240		
Gly	Ser	Ser	Cys	His	Arg	Arg	Leu	Ser	Asp	Gln	Asp	Pro	Gly	Ala	Asp		
				245					250					255			
Tyr	Gly	Gly	Gly	Lys	Arg	His	Arg										
			260														

<210> 755  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(2335)  
 <223> RXN02085

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 Met Thr Ser Asn Phe  
 1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg	163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	
10 15 20	
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
25 30 35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
40 45 50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
55 60 65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
70 75 80 85	
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883

Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507  
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
 1555  
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603  
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651  
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
 1699  
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747  
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795  
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843  
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
 570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga  
 1891  
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg  
 585 590 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc  
 1939  
 Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg  
 600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg  
 1987  
 Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met  
 615 620 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat  
 2035  
 Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp  
 630 635 640 645



gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc  
2083

Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu  
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg  
2131

Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val  
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt  
2179

Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc  
2227

Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct  
2275

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Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
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<213> Corynebacterium glutamicum

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Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
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Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
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Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu

100	105	110
Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu 115 120 125		
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala 130 135 140		
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg 145 150 155 160		
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr 165 170 175		
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr 180 185 190		
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu 195 200 205		
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg 210 215 220		
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr 225 230 235 240		
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly 245 250 255		
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu 260 265 270		
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly 275 280 285		
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Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val 325 330 335		
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu 340 345 350		
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala 355 360 365		
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met																	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
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 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
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 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
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 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
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 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
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 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
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 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
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 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
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 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
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 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
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 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
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Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
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 385 390 395 400  
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Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
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<211> 603

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 759

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Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
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Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
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Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
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603

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&lt;400&gt; 760

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Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
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Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
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&lt;210&gt; 761

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&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;223&gt; RXN02648

&lt;400&gt; 761

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Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val	
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Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala	
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Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
200					205					210						
tac	aag	atc	atc	acc	gat	gca	ggt	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	
215					220					225						
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys	
230					235					240					245	

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883  
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala  
                   250                                  255                                  260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931  
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly  
                   265                                  270                                  275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979  
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile  
                   280                                  285                                  290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca  
 1027  
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala  
                   295                                  300                                  305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt  
 1075  
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
 310                                  315                                  320                                  325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
 1123  
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
                   330                                  335                                  340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
 1171  
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
                   345                                  350                                  355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
 1219  
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
                   360                                  365                                  370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
 1267  
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
                   375                                  380                                  385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
 1313  
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 390                                  395                                  400

aacgaggggtt gct  
 1326

<210> 762

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
       1                                  5                                  10                                  15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
                   20                  25                  30  
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
                   35                  40                  45  
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
           50                  55                  60  
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
   65                  70                  75                  80  
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
                   85                  90                  95  
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
                  100                 105                 110  
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
          115                 120                 125  
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
   130                 135                 140  
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
  145                 150                 155                 160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
                  165                 170                 175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
                  180                 185                 190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
          195                 200                 205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
   210                 215                 220  
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
  225                 230                 235                 240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
                  245                 250                 255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
                  260                 265                 270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
          275                 280                 285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
   290                 295                 300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
  305                 310                 315                 320  
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
                  325                 330                 335  
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg

340						345						350					
Ile	Val	Gln	Phe	Ala	Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser		
355						360						365					
Thr	Asp	Cys	Gly	Leu	Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala		
370						375						380					
Lys	Leu	Glu	Ser	Leu	Val	Glu	Gly	Ala	Arg	Ile	Ala	Ser	Lys	Glu	Leu		
385						390						395					
390						395						400					
Phe																	

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<210> 763
<211> 548
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1) .. (525)
<223> FRXA02648

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<400> 763																	
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Asp	Ala	Pro	Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro		
1				5					10					15			
agc	gtg	aag	gat	tac	ttg	gac	tgg	atc	ggg	aca	cgc	atc	gat	gcc	atc	96	
Ser	Val	Lys	Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile		
			20					25					30				
aac	agt	gca	gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	144	
Asn	Ser	Ala	Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile		
		35					40					45					
tgc	tgg	ggc	tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggg	192	
Cys	Trp	Gly	Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly		
	50					55					60						
gac	atc	att	ggg	gag	atc	ctg	cgc	gca	gag	gtc	ggg	ggc	ttc	tcc	ttc	240	
Asp	Ile	Ile	Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe		
65					70					75					80		
gaa	ggc	gca	tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	288	
Glu	Gly	Ala	Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu		
				85					90					95			
aac	aag	ctt	cct	gaa	ggc	tct	gtt	atc	tac	cct	ggg	gtt	gtg	tct	cac	336	
Asn	Lys	Leu	Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His		
			100					105					110				
tcc	atc	aac	gct	gtg	gag	cac	cca	cgc	ctg	gtt	gct	gat	cgt	atc	gtt	384	
Ser	Ile	Asn	Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val		
		115					120					125					
cag	ttc	gcc	aag	ctt	gtt	ggc	cct	gag	aac	gtc	att	gcg	tcc	act	gac	432	
Gln	Phe	Ala	Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp		
	130					135					140						

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

taagctagac aacgagggtt gct 548

<210> 764

<211> 175

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 764

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro  
 1 5 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

<210> 765

<211> 784

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

&lt;400&gt; 765

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gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
                                   Met Ser Gln Asn Arg
                                   1      5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
              10              15              20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
              25              30              35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
              40              45              50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
              55              60              65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
              70              75              80              85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
              90              95              100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
              105              110              115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
              120              125              130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
              135              140              145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
              150              155              160              165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
              170              175              180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
              185              190              195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
              200              205              210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784

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Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220

Gln Leu Asp Ala  
 225

<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(490)

&lt;223&gt; RXA01516

&lt;400&gt; 767

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tctgcacata tgggagcatg ggggtgtgcgc gtgcacgatg tcccagtatc aagggacgct 60

gtt gatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115
              Met Ala Asp Arg Ile
              1 5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
              10 15 20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
              25 30 35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
              40 45 50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
              55 60 65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
              70 75 80 85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
              90 95 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
              105 110 115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
              120 125 130

agttttgtcc atc 513

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&lt;210&gt; 768

&lt;211&gt; 130

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 768

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Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
  1 5 10 15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
  20 25 30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
  35 40 45

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Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile  
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser  
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val  
 85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val  
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser  
 115 120 125

Asn Ala  
 130

<210> 769  
 <211> 975  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(952)  
 <223> RXA01515

<400> 769  
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ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115  
 Met Asn Val Ser Ser  
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163  
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211  
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala  
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259  
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp  
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307  
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser  
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355  
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala  
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403  
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala  
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451  
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu  
 105 110 115  
  
 gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499  
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val  
 120 125 130  
  
 tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547  
 Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln  
 135 140 145  
  
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595  
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp  
 150 155 160 165  
  
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643  
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile  
 170 175 180  
  
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691  
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp  
 185 190 195  
  
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739  
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile  
 200 205 210  
  
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787  
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp  
 215 220 225  
  
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835  
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala  
 230 235 240 245  
  
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883  
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His  
 250 255 260  
  
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931  
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg  
 265 270 275  
  
 agt gga gga act cac cat ggc tgatcgatt gaacttaaag gcc 975  
 Ser Gly Gly Thr His His Gly  
 280

&lt;210&gt; 770

&lt;211&gt; 284

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly  
 1 5 10 15

Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile  
 20 25 30

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly  
                   35                                  40                                  45  
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val  
                   50                                  55                                  60  
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys  
                   65                                  70                                  75                                  80  
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
                                   85                                  90                                  95  
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
                                   100                                  105                                  110  
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu  
                   115                                  120                                  125  
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
                   130                                  135                                  140  
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
                   145                                  150                                  155                                  160  
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
                                   165                                  170                                  175  
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
                                   180                                  185                                  190  
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser  
                   195                                  200                                  205  
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala  
                   210                                  215                                  220  
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
                   225                                  230                                  235                                  240  
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp  
                                   245                                  250                                  255  
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val  
                   260                                  265                                  270  
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly  
                   275                                  280

&lt;210&gt; 771

&lt;211&gt; 859

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(859)

&lt;223&gt; RXA02024

&lt;400&gt; 771

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	Met Ser Ser Leu Pro	
	1 5	
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Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys		
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Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val		
25 30 35		
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Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly		
40 45 50		
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307	
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro		
55 60 65		
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355	
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val		
70 75 80 85		
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403	
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala		
90 95 100		
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451	
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln		
105 110 115		
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499	
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly		
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gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547	
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val		
135 140 145		
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595	
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg		
150 155 160 165		
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643	
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe		
170 175 180		
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691	
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu		
185 190 195		
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739	
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp		
200 205 210		
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Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly		
215 220 225		

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835  
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cgc gtg cat gaa gtt gcg gaa acc 859  
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<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

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Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly  
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile  
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp  
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala  
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp  
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys  
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His  
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala  
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp  
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu  
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala  
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp  
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Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr

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250

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<223> RXA01719
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																											1						
ctt	gct	gg	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	163									
Leu	Ala	Gly	Gly	Glu	Gly	Lys	Arg	Met	Gly	Gly	Val	Asp	Lys	Ala	Ala																		
																											10				20		
gtg	gcg	gtg	gat	gg	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	211									
Val	Ala	Val	Asp	Gly	Arg	Thr	Leu	Leu	Asp	Ile	Leu	Leu	Ser	Gln	Leu																		
																											25				35		
gat	cca	gaa	gat	gac	gtc	gtg	gtg	gtt	tcc	ccc	gcg	atc	atc	gac	gga								259										
Asp	Pro	Glu	Asp	Asp	Val	Val	Val	Val	Ser	Pro	Ala	Ile	Ile	Asp	Gly																		
																											40				50		
atc	acg	act	gtc	tgc	gag	gaa	cct	ccg	ctt	ggc	ggg	ccg	gtc	gcg	gga								307										
Ile	Thr	Thr	Val	Cys	Glu	Glu	Pro	Pro	Leu	Gly	Gly	Pro	Val	Ala	Gly																		
																											55				60		
atc	gag	gca	ggg	ctg	aat	tct	ttt	gag	cac	gcc	cat	gaa	ttc	act	gcg								355										
Ile	Glu	Ala	Gly	Leu	Asn	Ser	Phe	Glu	His	Ala	His	Glu	Phe	Thr	Ala																		
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att	ctt	gcc	gtg	gac	gcg	cct	tat	tct	gca	gcg	atg	ctg	ccc	cta	ctt								403										
Ile	Leu	Ala	Val	Asp	Ala	Pro	Tyr	Ser	Ala	Ala	Met	Leu	Pro	Leu	Leu																		
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cag	gca	cag	att	ggc	aaa	gcc	gat	gtg	gcc	gta	acc	ctt	gct	gcc	gat								451										
Gln	Ala	Gln	Ile	Gly	Lys	Ala	Asp	Val	Ala	Val	Thr	Leu	Ala	Ala	Asp																		
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ggc	tgg	gta	caa	ccg	ttg	tgc	gcg	ctg	tgg	aga	agt	ggc	agc	cta	gaa								499										
Gly	Trp	Val	Gln	Pro	Leu	Cys	Ala	Leu	Trp	Arg	Ser	Gly	Ser	Leu	Glu																		
																											120				125		
gcg	gtg	att	cac	agc	ctg	ggc	gag	act	aga	aat	cga	ccg	gca	aaa	gcg								547										
Ala	Val	Ile	His	Ser	Leu	Gly	Glu	Thr	Arg	Asn	Arg	Pro	Ala	Lys	Ala																		
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tta	ctg	aag	caa	gcg	gga	cac	att	gtg	gaa	gtg	ggg	ggc	gat	ggc	act								595										
Leu	Leu	Lys	Gln	Ala	Gly	His	Ile	Val	Glu	Val	Gly	Gly	Asp	Gly	Thr																		
																											150				155		
gaa	aaa	gac	tac	gat	acg	gtg	gct	gaa	ctg	aaq	gta	ttg	ggc	aac	gta								643										



Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val  
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acg ctc cct aaa gcc cac tgatgagaaa cgtgagctct gct 684  
 Thr Leu Pro Lys Ala His  
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<210> 774  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 774  
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 Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro  
 35 40 45  
 Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly  
 50 55 60  
 Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala  
 65 70 75 80  
 His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala  
 85 90 95  
 Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val  
 100 105 110  
 Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg  
 115 120 125  
 Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn  
 130 135 140  
 Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val  
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                               Val Ala Gln Gln Arg
                               1           5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
                10                15                20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
                25                30                35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
                40                45                50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
                55                60                65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
                70                75                80                85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
                90                95                100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr
                105                110                115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu
                120                125                130

cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys
                135                140                145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr
                150                155                160                165

gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct 643
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro
                170                175                180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly
                185                190                195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu
                200                205                210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp

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215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg			835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala			
230	235	240	245
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg			883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val			
	250	255	260
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att			931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile			
	265	270	275
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca			979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala			
	280	285	290
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt			
1027			
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe			
	295	300	305
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg			
1075			
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg			
310	315	320	325
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg			
1123			
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg			
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gcg ctg aag gcg ccg gag ggc ccc gta ttg gcg ata ccg gtg gcg att			
1171			
Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile			
	345	350	355
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg			
1219			
Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met			
	360	365	370
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg			
1267			
Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser			
	375	380	385
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg			
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Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met			
390	395	400	
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1332			
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<213> Corynebacterium glutamicum			

&lt;400&gt; 776

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 Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro  
 35 40 45  
 Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp  
 50 55 60  
 Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro  
 65 70 75 80  
 Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val  
 85 90 95  
 Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val  
 100 105 110  
 Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu  
 115 120 125  
 Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala  
 130 135 140  
 Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala  
 145 150 155 160  
 Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr  
 165 170 175  
 Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp  
 180 185 190  
 Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro  
 195 200 205  
 Met Leu Val Ala Glu Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His  
 210 215 220  
 Phe His Ser Asp Asp Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys  
 225 230 235 240  
 Pro Ala Glu Val Ala Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala  
 245 250 255  
 Gly Ala Phe Asp Val Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe  
 260 265 270  
 Glu Phe Phe Pro Ile Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly  
 275 280 285  
 Gln Trp Gly Asp Ala Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala  
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 Ala Trp Val Ser Phe Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu  
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Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala			
			20					25					30					
gcg	att	gat	ggt	tat	gcg	gtt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag		145	
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys			
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Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro			
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gtg	gtg	ggt	gaa	gta	gct	gcg	ggt	tct	cag	cag	ccg	ttg	cgc	ctg	cag		241	
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln			
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cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggt	gcg	cca	ctg	ccg	atg	ctt		289	
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu			
			85						90					95				
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga		337	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg			
			100					105					110					
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa		385	
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu			

115	120	125	
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Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val			
130	135	140	
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa			481
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys			
145	150	155	160
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct			529
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala			
	165	170	175
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat			577
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp			
	180	185	190
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat			625
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp			
	195	200	205
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag			673
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu			
	210	215	220
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga			721
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly			
	225	230	235
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag			769
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu			
	245	250	255
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc			817
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val			
	260	265	270
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg			865
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu			
	275	280	285
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc			913
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg			
	290	295	300
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt			961
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val			
	305	310	315
ggt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa			1009
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys			
	325	330	335
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac			1057
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr			
	340	345	350

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg  
1105

Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu  
355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc  
1153

Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val  
370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa  
1201

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln  
385 390 395 400

ggt cga tagttcgatg cgtaatgcac cgtcagggtcc  
1237

Gly Arg

<210> 778

<211> 402

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 778

Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys  
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Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala  
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Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys  
35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro  
50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln  
65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu  
85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg  
100 105 110

Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu  
115 120 125

Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val  
130 135 140

Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys  
145 150 155 160

Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala  
165 170 175

Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp

[illegible]

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<210> 779
<211> 1229
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1) .. (1206)  
<223> FRXA01970
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<400> 779  
cca gag cca gtg cgt att gct att gca gag gca ctg ggt ttg atg tgc 48  
Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys  
1 5 10 15  
gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 96



Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala		
			20					25					30				
gcg	att	gat	ggg	tat	gcg	gtt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag	144	
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys		
		35					40					45					
tcg	ttt	agc	cag	caa	ctg	ccg	gtt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	192	
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro		
		50				55					60						
gtg	gtg	ggg	gaa	gta	gct	gcg	ggg	tct	cag	cag	ccg	ttg	cgc	ctg	cag	240	
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln		
	65				70				75						80		
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggg	gcg	cca	ctg	ccg	atg	ctt	288	
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu		
			85					90						95			
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	336	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg		
			100					105					110				
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa	384	
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu		
		115					120					125					
ggc	gat	gac	atc	caa	ccg	gga	gac	atc	gca	gtc	agc	gcc	ggc	gcg	gtc	432	
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val		
	130					135					140						
tta	ggc	cct	gcc	caa	att	ggg	ttg	ctc	gca	gct	gtt	ggg	cgc	tcc	aaa	480	
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys		
	145				150					155					160		
gtg	ttg	gtg	tac	cca	cgc	cca	cgc	atg	tcg	gtt	atc	tcc	gta	ggc	gct	528	
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala		
				165					170					175			
gaa	ctt	gtt	gat	att	gat	cgc	cag	cca	ggc	ctc	ggc	cag	gtt	tat	gat	576	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp		
			180					185					190				
gtc	aat	tcc	tat	tct	ctg	gct	gcc	gcc	ggg	agg	gaa	gcg	ggc	gca	gat	624	
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
		195					200					205					
gtg	tac	cgc	tac	ggc	att	gct	gcc	ggg	gaa	cct	cgt	cgc	atc	aaa	gag	672	
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
	210					215					220						
atc	att	gaa	tcc	cag	atg	ctg	cgc	tcg	gaa	atc	atc	gtc	atc	acc	gga	720	
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
	225				230					235					240		
gct	gtt	ggc	ggg	gct	ggg	tca	gct	ggc	gtg	cgc	cag	gtt	ctc	aac	gag	768	
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
				245					250					255			
cta	ggc	gat	atc	gac	acc	gaa	cgc	gtc	gca	atg	cac	ccc	ggg	tct	gtc	816	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		

260	265	270	
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg			864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu			
275	280	285	
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc			912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg			
290	295	300	
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt			960
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val			
305	310	315	320
ggt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa			
1008			
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys			
325	330	335	
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac			
1056			
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr			
340	345	350	
ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg			
1104			
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu			
355	360	365	
gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc			
1152			
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val			
370	375	380	
aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa			
1200			
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln			
385	390	395	400
ggt cga tagttcgatg cgtaatgcac cgt			
1229			
Gly Arg			

&lt;210&gt; 780

&lt;211&gt; 402

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 780

Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys
1				5					10					15	

Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
			20					25					30		

Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys
		35					40					45			

Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60					
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln
65					70					75					80
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu
				85					90					95	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg
			100					105						110	
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
			115					120						125	
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130					135						140			
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145						150				155					160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
				165					170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185						190	
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
			195				200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215						220			
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225						230				235					240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
						295						300			
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305						310				315					320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
				325					330					335	
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340					345					350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
						375						380			

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln  
 385 390 395 400

Gly Arg

<210> 781

<211> 708

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(685)

<223> RXA02629

<400> 781

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atctgcatct aatcaagtag ccaagtatga gtgaggaaca atg agc aag gat cca 115
Met Ser Lys Asp Pro
1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu
55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
120 125 130

gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
135 140 145
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tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595  
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu  
 150 155 160 165

gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643  
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro  
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685  
 Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr Ser Val Val  
 185 190 195

tgagttgggc ggggtgtgagt aga 708

<210> 782

<211> 195

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 782

Met Ser Lys Asp Pro Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg  
 1 5 10 15

Val Pro Leu Pro Asp Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr  
 20 25 30

Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu  
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr  
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val  
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val  
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro  
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val  
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala  
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr  
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met  
 165 170 175

Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr  
 180 185 190

Ser Val Val  
 195

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<210> 783
<211> 402
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(379)
<223> RXA02318
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<210> 784
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<212> PRT
<213> Corynebacterium glutamicum
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Met Asn Ser Leu Phe Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala
 1             5             10             15

Lys Leu Thr Ala His Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys
      20             25             30

Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro
      35             40             45

Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His
 50             55             60

Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile

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65	70	75	80
Asp Ala His Ala Lys Thr Leu Ala Ile Ser Ala Glu Ala			
	85	90	
 <210> 785			
<211> 600			
<212> DNA			
<213> Corynebacterium glutamicum			
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<222> (101)..(577)			
<223> RXA01517			
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ggtccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg	115		
	Met His Ala Val Leu		
	1	5	
tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg	163		
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val			
	10	15	20
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca	211		
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser			
	25	30	35
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg	259		
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val			
	40	45	50
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc	307		
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly			
	55	60	65
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg	355		
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly			
	70	75	80
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa	403		
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu			
	90	95	100
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct	451		
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala			
	105	110	115
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat	499		
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp			
	120	125	130
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat	547		
Ala Val Leu His Gly Thr Ile Ala Glu His Val Asp Asn Leu Asp			
	135	140	145
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat	597		
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile			

150

155

gca

600

&lt;210&gt; 786

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 786

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala  
 1 5 10 15

Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln  
 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu  
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu  
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg  
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile  
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu  
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu  
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His  
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile  
 145 150 155

&lt;210&gt; 787

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(586)

&lt;223&gt; RXN01304

&lt;400&gt; 787

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tgaaaaaggg gattaattac cccacttga ggagaaattg atg ccc gca cag aac 115  
 Met Pro Ala Gln Asn  
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163  
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser



	10	15	20	
gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag				211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln				
	25	30	35	
gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt				259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe				
	40	45	50	
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc				307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg				
	55	60	65	
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg				355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr				
	70	75	80	85
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg				403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met				
	90	95	100	
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta				451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu				
	105	110	115	
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc				499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu				
	120	125	130	
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg				547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly				
	135	140	145	
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt				596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu				
	150	155	160	
ttgcttatcg acg				609
<210> 788				
<211> 162				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 788				
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1 5 10 15				
Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala				
20 25 30				
Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val				
35 40 45				
Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu				
50 55 60				
Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly				
65 70 75 80				

[illegible]

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<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1258)
<223> RXS02556
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											ttg	atc	gtt	tcc	acc	
											Leu	Ile	Val	Ser	Thr	
											1				5	
cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg																163
Gln	Pro	Ile	Thr	Asp	Arg	Ser	Ala	Leu	Ser	Ala	Glu	His	Ala	Glu	Val	
				10					15					20		
atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg																211
Ile	Lys	Ala	Thr	Leu	Pro	Leu	Val	Gly	Gly	Lys	Ile	Asn	Glu	Ile	Thr	
			25					30					35			
ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct																259
Pro	Val	Phe	Tyr	Asn	Lys	Met	Phe	Ala	Ala	His	Pro	Glu	Leu	Ile	Ala	
		40					45					50				
aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg																307
Asn	Thr	Phe	Asn	Arg	Gly	Asn	Gln	Lys	Gln	Gly	Asp	Gln	Gln	Lys	Ala	
	55					60					65					
ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat																355
Leu	Ala	Ala	Ser	Ile	Ala	Thr	Phe	Ala	Thr	Met	Leu	Val	Thr	Pro	Asp	
70					75					80					85	
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg																403
Ala	Pro	Asp	Pro	Val	Gln	Leu	Leu	Ser	Arg	Ile	Gly	His	Lys	His	Val	
				90					95				100			

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg	451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	
105 110 115	
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct	499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	
120 125 130	
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg	547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	
135 140 145	
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc	595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	
150 155 160 165	
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca	643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	
170 175 180	
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca	691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	
185 190 195	
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag	739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	
200 205 210	
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att	787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	
215 220 225	
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta	835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	
230 235 240 245	
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt	883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	
250 255 260	
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc	931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	
265 270 275	
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac	979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	
280 285 290	
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg	
1027	
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	
295 300 305	
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa	
1075	
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu	
310 315 320 325	
atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att	
1123	
Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile	

330 335 340  
 cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag  
 1171  
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys  
 345 350 355  
 aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta  
 1219  
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val  
 360 365 370  
 aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca  
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 <210> 790  
 <211> 386  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 790  
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 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
 35 40 45  
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly  
 50 55 60  
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
 65 70 75 80  
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
 85 90 95  
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
 100 105 110  
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
 115 120 125  
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
 130 135 140  
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
 145 150 155 160  
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
 165 170 175  
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu

180					185					190					
Val	Ala	Pro	Glu	Pro	Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp
		195					200					205			
Asp	Gly	Ala	Arg	Gln	Leu	Arg	Gln	Tyr	Ser	Leu	Leu	Gly	Gly	Ser	Asp
	210					215					220				
Thr	Glu	Tyr	Arg	Ile	Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe
225					230					235					240
Leu	Arg	Asp	Arg	Val	Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala
			245						250					255	
Ala	Gly	Asp	Leu	Val	Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile
		260						265					270		
Ser	Gln	Gly	Ile	Gly	Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met
	275						280					285			
Asn	Pro	Glu	Arg	Asp	Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser
	290					295					300				
Thr	Tyr	Ala	Gln	Val	Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro
305					310					315					320
Lys	Ala	Ala	Phe	Glu	Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu
			325						330					335	
Val	Ala	Gly	Arg	Ile	Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly
			340					345					350		
Val	Glu	Phe	Leu	Lys	Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu
	355						360					365			
Gln	Pro	Arg	Asp	Val	Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu
	370					375					380				
Ile	Ser														
385															

&lt;210&gt; 791

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(967)

&lt;223&gt; RXS02560

&lt;400&gt; 791

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ggaacttcta	agagcagtg	aatgaaataa	tccggtgctg	atg	cag	ggc	aac	tcg	115
				Met	Gln	Gly	Asn	Ser	
				1				5	

ctt	aat	ctg	gca	gac	aac	agc	gag	aga	aag	aag	ccc	atg	ccg	tca	cca	163
Leu	Asn	Leu	Ala	Asp	Asn	Ser	Glu	Arg	Lys	Lys	Pro	Met	Pro	Ser	Pro	

10								15				20				
gga	gaa	ctt	tta	gcc	gcc	cgc	tac	gga	caa	cct	gca	acc	tgg	acg	cca	211
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro	
25				30				35								
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val	
40				45				50								
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile	
55				60				65								
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile	
70				75				80				85				
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
90				95				100								
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
105				110				115								
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu	
120				125				130								
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg	547
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly	
135				140				145								
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag	595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu	
150				155				160				165				
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggt	tcg	gtg	cgc	aac	gat	gcg	643
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala	
170				175				180								
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc	691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val	
185				190				195								
gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att	739
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile	
200				205				210								
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc	787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr	
215				220				225								
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act	835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr	
230				235				240				245				
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg	883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala	
250				255				260								

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931  
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu  
                   265                                  270                                  275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977  
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg  
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attatggacg cct 990

<210> 792

<211> 289

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 792

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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro  
                   20                                  25                                  30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  
                   35                                  40                                  45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp  
           50                                  55                                  60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser  
           65                                  70                                  75                                  80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg  
                   85                                  90                                  95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln  
                   100                                  105                                  110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala  
           115                                  120                                  125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp  
           130                                  135                                  140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala  
           145                                  150                                  155                                  160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser  
                   165                                  170                                  175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro  
                   180                                  185                                  190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro  
           195                                  200                                  205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His  
           210                                  215                                  220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp

225		230		235		240									
Arg	Ala	Leu	Asp	Thr	Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp
			245						250					255	
Ser	Lys	Gln	Thr	Ala	His	Arg	Ala	Ala	Ser	Lys	Ser	Phe	Ser	Lys	Thr
			260					265					270		
Asn	Arg	Gln	Phe	Leu	Arg	Gly	Val	Phe	Glu	Arg	Ala	Gly	Phe	Gly	Leu
		275					280					285			

Arg

&lt;210&gt; 793

&lt;211&gt; 1425

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1402)

&lt;223&gt; RXA00382

&lt;400&gt; 793

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				Met	Thr	Ser	Ser	Asn	
				1				5	

acg	gct	cga	tcc	gca	gag	tgg	ttt	gaa	aag	gct	cag	aag	ctc	acc	cct	163
Thr	Ala	Arg	Ser	Ala	Glu	Trp	Phe	Glu	Lys	Ala	Gln	Lys	Leu	Thr	Pro	
			10					15					20			

ggt	ggt	gtg	aat	tct	cct	ggt	cgc	gct	ttc	ggt	tca	gtt	ggc	gga	caa	211
Gly	Gly	Val	Asn	Ser	Pro	Val	Arg	Ala	Phe	Gly	Ser	Val	Gly	Gly	Gln	
		25					30						35			

gcc	cgt	ttc	atc	gaa	aaa	gct	cac	ggt	tca	acg	ctg	atc	gat	gtg	gac	259
Ala	Arg	Phe	Ile	Glu	Lys	Ala	His	Gly	Ser	Thr	Leu	Ile	Asp	Val	Asp	
		40					45					50				

gga	aat	gaa	tac	gtt	gac	ctg	gtc	tgt	tct	tgg	ggc	ccc	atg	ctg	atg	307
Gly	Asn	Glu	Tyr	Val	Asp	Leu	Val	Cys	Ser	Trp	Gly	Pro	Met	Leu	Met	
	55					60					65					

ggt	cac	gct	cac	cca	gca	gtg	gtc	gag	gct	gtg	cag	aag	gcc	gtc	gtg	355
Gly	His	Ala	His	Pro	Ala	Val	Val	Glu	Ala	Val	Gln	Lys	Ala	Val	Val	
	70				75				80					85		

gat	ggt	ctt	tct	ttc	ggc	gct	ccc	acc	atc	ggt	gag	gtt	gag	ttg	gcc	403
Asp	Gly	Leu	Ser	Phe	Gly	Ala	Pro	Thr	Ile	Gly	Glu	Val	Glu	Leu	Ala	
			90					95						100		

caa	gat	atc	gtc	aag	cgc	act	tct	gtg	gag	gaa	gtc	cgc	ctg	gtc	aac	451
Gln	Asp	Ile	Val	Lys	Arg	Thr	Ser	Val	Glu	Glu	Val	Arg	Leu	Val	Asn	
		105						110					115			

tcc	ggc	act	gag	gcc	acc	atg	tcg	gcg	gtt	cgt	ctg	gcg	cgc	ggt	tac	499
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



Ser	Gly	Thr	Glu	Ala	Thr	Met	Ser	Ala	Val	Arg	Leu	Ala	Arg	Gly	Tyr		
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act	cag	cgt	tcc	aag	att	ttg	aag	ttt	gag	ggc	tgc	tac	cac	ggc	cac	547	
Thr	Gln	Arg	Ser	Lys	Ile	Leu	Lys	Phe	Glu	Gly	Cys	Tyr	His	Gly	His		
		135				140					145						
gtc	gat	gcg	ctg	ctc	gca	tct	gct	ggc	tct	ggc	gtc	gca	act	ttc	gct	595	
Val	Asp	Ala	Leu	Leu	Ala	Ser	Ala	Gly	Ser	Gly	Val	Ala	Thr	Phe	Ala		
		150			155					160					165		
ctg	cct	gat	tcc	cca	ggc	atc	acc	ggc	gct	cag	act	tct	gac	act	att	643	
Leu	Pro	Asp	Ser	Pro	Gly	Ile	Thr	Gly	Ala	Gln	Thr	Ser	Asp	Thr	Ile		
				170					175					180			
gtt	gtt	cct	tac	aac	gac	att	gaa	gcc	gtg	cgc	aac	gct	ttt	gcg	gag	691	
Val	Val	Pro	Tyr	Asn	Asp	Ile	Glu	Ala	Val	Arg	Asn	Ala	Phe	Ala	Glu		
			185					190						195			
tac	cca	ggc	gag	atc	gcc	tgc	atc	atc	gca	gag	gca	gcc	ggc	ggc	aac	739	
Tyr	Pro	Gly	Glu	Ile	Ala	Cys	Ile	Ile	Ala	Glu	Ala	Ala	Gly	Gly	Asn		
		200					205					210					
atg	ggc	acc	gtc	gct	cca	aag	gac	aac	ttt	aac	gac	aag	ctt	ctc	gcg	787	
Met	Gly	Thr	Val	Ala	Pro	Lys	Asp	Asn	Phe	Asn	Asp	Lys	Leu	Leu	Ala		
		215				220					225						
atc	gct	cac	gct	gac	ggc	gcg	ctg	ctg	atc	ctc	gat	gaa	gtc	atg	acc	835	
Ile	Ala	His	Ala	Asp	Gly	Ala	Leu	Leu	Ile	Leu	Asp	Glu	Val	Met	Thr		
		230			235					240					245		
ggc	ttc	cgc	acc	tct	tac	cgt	ggc	tgg	ttc	ggc	gta	gac	aag	gtt	gcc	883	
Gly	Phe	Arg	Thr	Ser	Tyr	Arg	Gly	Trp	Phe	Gly	Val	Asp	Lys	Val	Ala		
				250				255						260			
gct	gac	ctg	gtc	acc	ttc	ggc	aag	gtc	gtc	tcc	ggc	ggc	cta	cct	gcc	931	
Ala	Asp	Leu	Val	Thr	Phe	Gly	Lys	Val	Val	Ser	Gly	Gly	Leu	Pro	Ala		
			265					270					275				
gca	gcg	ttt	ggc	ggc	aag	gct	gaa	atc	atg	aac	atg	ctg	gcc	cca	cag	979	
Ala	Ala	Phe	Gly	Gly	Lys	Ala	Glu	Ile	Met	Asn	Met	Leu	Ala	Pro	Gln		
		280					285					290					
ggc	ccc	gtc	tac	caa	gca	ggc	aca	ctg	tcc	ggc	aac	ccg	gtt	gcg	gtc		
		1027															
Gly	Pro	Val	Tyr	Gln	Ala	Gly	Thr	Leu	Ser	Gly	Asn	Pro	Val	Ala	Val		
		295				300					305						
gca	gct	ggc	cgg	gca	tcg	ctt	aag	ctt	gcc	gac	gaa	tcc	ctc	tac	aca		
		1075															
Ala	Ala	Gly	Arg	Ala	Ser	Leu	Lys	Leu	Ala	Asp	Glu	Ser	Leu	Tyr	Thr		
		310			315					320					325		
acc	atc	aac	gcc	aac	gca	gat	cgt	ctc	cac	ggc	ttg	atc	tct	gat	gcc		
		1123															
Thr	Ile	Asn	Ala	Asn	Ala	Asp	Arg	Leu	His	Gly	Leu	Ile	Ser	Asp	Ala		
				330					335					340			
tta	acc	cac	gaa	ggc	gta	gcc	cac	cac	att	cag	cgt	gcc	tca	aac	atg		
		1171															
Leu	Thr	His	Glu	Gly	Val	Ala	His	His	Ile	Gln	Arg	Ala	Ser	Asn	Met		

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 1219  
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 aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg  
 1267  
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu  
 375 380 385  
 gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg  
 1315  
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val  
 390 395 400 405  
 tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc  
 1363  
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu  
 410 415 420  
 aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac  
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 Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys Ala Ser  
 425 430  
 cattgtccat cta  
 1425

&lt;210&gt; 794

&lt;211&gt; 434

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 794

Met Thr Ser Ser Asn Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala  
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 Gln Lys Leu Thr Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly  
 20 25 30  
 Ser Val Gly Gly Gln Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr  
 35 40 45  
 Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp  
 50 55 60  
 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val  
 65 70 75 80  
 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly  
 85 90 95  
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu  
 100 105 110  
 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg  
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly  
 130 135 140  
 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly  
 145 150 155 160  
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln  
 165 170 175  
 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg  
 180 185 190  
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu  
 195 200 205  
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn  
 210 215 220  
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu  
 225 230 235 240  
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly  
 245 250 255  
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser  
 260 265 270  
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn  
 275 280 285  
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly  
 290 295 300  
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp  
 305 310 315 320  
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly  
 325 330 335  
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln  
 340 345 350  
 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His  
 355 360 365  
 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe  
 370 375 380  
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe  
 385 390 395 400  
 Glu Thr Trp Phe Val Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys  
 405 410 415  
 Ile Glu Gln Ala Leu Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys  
 420 425 430  
 Ala Ser



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gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat 691
Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn
185 190 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835
Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
280 285 290

atg gtg gtc gag cgt gtc gct acc gtt ggc ccc acc gat gaa ttc gca
1027
Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc
1075
Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
310 315 320 325

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca
1123
Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg
1171
Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat
1220
Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn
360 365 370

agtcacctcgc aaa
1233

```

&lt;210&gt; 796

&lt;211&gt; 370

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 796

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Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser
 1              5              10              15

Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn
      20              25              30

Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
      35              40              45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
 50              55              60

Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
 65              70              75              80

Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
      85              90              95

Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
      100              105              110

Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
      115              120              125

Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
      130              135              140

Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
      145              150              155              160

Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
      165              170              175

Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
      180              185              190

Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
      195              200              205

Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
      210              215              220

Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
      225              230              235              240

Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
      245              250              255

Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
      260              265              270

Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
      275              280              285

Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
      290              295              300

Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
      305              310              315              320

```

Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser  
325 330 335

Ser Val Asn Gly Ala Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys  
340 345 350

His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala  
355 360 365

Ala Asn  
370

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<210> 797
<211> 810
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXA00624
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<400> 797																	
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caacaggacg	acaacggccg	gacatgcgac	aatacaatgc	atg	tcc	ggc	cgt	ctt									115
				Met	Ser	Gly	Arg	Leu									5
				1													
ctt	gtt	tca	gtt	tct	agt	att	ttc	gac	cag	acc	cga	tcg	gcg	gct	gac		163
Leu	Val	Ser	Val	Ser	Ser	Ile	Phe	Asp	Gln	Thr	Arg	Ser	Ala	Ala	Asp		
				10												20	
agg	ctc	att	tca	gac	ctg	cga	gcc	gac	ggc	atc	gag	gtc	tca	tta	ctt		211
Arg	Leu	Ile	Ser	Asp	Leu	Arg	Ala	Asp	Gly	Ile	Glu	Val	Ser	Leu	Leu		
			25												30	35	
gtc	gca	ccc	cgc	atc	gat	ggg	gac	tgg	cgt	ctc	gcc	aaa	gac	aaa	ggg		259
Val	Ala	Pro	Arg	Ile	Asp	Gly	Asp	Trp	Arg	Leu	Ala	Lys	Asp	Lys	Gly		
		40												45	50		
acc	ctc	gcg	tgg	atg	gaa	caa	caa	cgc	gaa	cgc	ggc	cac	gaa	ctc	atc		307
Thr	Leu	Ala	Trp	Met	Glu	Gln	Gln	Arg	Glu	Arg	Gly	His	Glu	Leu	Ile		
	55												60	65			
ctc	aac	ggt	ttc	gac	caa	gca	gtt	cag	gga	cgt	cgc	tca	gaa	ttc	gcc		355
Leu	Asn	Gly	Phe	Asp	Gln	Ala	Val	Gln	Gly	Arg	Arg	Ser	Glu	Phe	Ala		
	70												75	80	85		
aac	ctt	gaa	cgg	cac	gaa	gca	cgt	ctt	cgc	ctt	acc	ggt	gcc	att	agg		403
Asn	Leu	Glu	Arg	His	Glu	Ala	Arg	Leu	Arg	Leu	Thr	Gly	Ala	Ile	Arg		
			90												95	100	
caa	atg	cag	aaa	att	ggc	ttc	gaa	ttc	caa	atc	ttt	gcc	cca	cct	cgt		451
Gln	Met	Gln	Lys	Ile	Gly	Phe	Glu	Phe	Gln	Ile	Phe	Ala	Pro	Pro	Arg		
			105												110	115	
tgg	aga	atg	tca	gaa	ggc	acc	ttc	gcg	gta	ctc	cca	gaa	ttt	gat	ttc		499
Trp	Arg	Met	Ser	Glu	Gly	Thr	Phe	Ala	Val	Leu	Pro	Glu	Phe	Asp	Phe		

120	125	130	
aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa			547
Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
135	140	145	
ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca			595
Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
150	155	160	165
aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
	170	175	180
aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac			691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
	185	190	195
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp			
	200	205	210
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala			
	215	220	225
tagttgggga gggttcggggc acc			810

&lt;210&gt; 798

&lt;211&gt; 229

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 798

Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr
1 5 10 15

Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile
20 25 30

Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu
35 40 45

Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg
50 55 60

Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg
65 70 75 80

Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu
85 90 95

Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile
100 105 110

Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu
115 120 125

Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn
130 135 140



Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu  
 145 150 155 160  
 Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val  
 165 170 175  
 Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala  
 180 185 190  
 Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala  
 195 200 205  
 Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala  
 210 215 220  
 Ala Ala Gln Leu Ala  
 225

<210> 799  
 <211> 956  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(933)  
 <223> RXA00306

<400> 799  
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 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15  
 gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30  
 gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45  
 cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192  
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60  
 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240  
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80  
 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288  
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95  
 tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336  
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110  
 gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384  
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

115	120	125	
gca gca gca cgc acc acc	gcg tgg ctt aac cac ttt	gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr	Ala Trp Leu Asn His Phe	Glu Lys Ala Lys	
130	135	140	
gtt caa ggc gtt ggt ttt	ggt ttc atc gcc atc caa	cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe	Gly Phe Ile Ala Ile Gln	Arg Leu Glu Glu	
145	150	155 160	
gac gag gcg gat gag aaa	tcc gat atc ttg gct gaa	tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys	Ser Asp Ile Leu Ala Glu	Ser Met Thr Gln	
165	170	175	
tac ttc gag gat cct ctc	ggc cct gaa att gag gag	tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu	Gly Pro Glu Ile Glu Glu	Tyr Phe Thr Arg	
180	185	190	
acc gca tgg ctt cgt gaa	caa act cgc gat tcc att	ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu	Gln Thr Arg Asp Ser Ile	Leu Ser Ser Arg	
195	200	205	
ttc aaa gtt cgc cct ggc	gtg gcc cgg gaa caa atc	agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly	Val Ala Arg Glu Gln Ile	Ser Leu Ala Asp	
210	215	220	
gcg gaa gaa ggc atg ggc	ttt agt cct gtc acg ttg	agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly	Phe Ser Pro Val Thr Leu	Arg Leu Thr Arg	
225	230	235 240	
acc gat ggt cct cgt tgg	tcc cat gat gtt gat gag	cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp	Ser His Asp Val Asp Glu	His Val Ala Ser	
245	250	255	
atc gtc gca gga ctt aac	cca cat gga ctc ccc ttt	gaa gaa atc ctg	816
Ile Val Ala Gly Leu Asn	Pro His Gly Leu Pro Phe	Glu Glu Ile Leu	
260	265	270	
gaa atg tac gcg atg gct	caa ggt atc gag gga gaa	tcc ctg cac aac	864
Glu Met Tyr Ala Met Ala	Gln Gly Ile Glu Gly Glu	Ser Leu His Asn	
275	280	285	
ggc gcc att gcg gcg ttg	gtg gat ctc atc cgc cac	gga ttg gtg ttg	912
Gly Ala Ile Ala Ala Leu	Val Asp Leu Ile Arg His	Gly Leu Val Leu	
290	295	300	
ccc gct gat ctt ctc gat	tct taaataagga ctgattgtga	aag	956
Pro Ala Asp Leu Leu Asp	Ser		
305	310		
<210> 800			
<211> 311			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 800			
Asp Ser Gly Ile Pro Thr	Gln Leu Val Glu Gly Ser Trp	Phe Glu Pro	
1	5	10 15	
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val			

20										25					30															
Val	Gly	Pro	Pro	Glu	Ile	Gly	His	Val	Tyr	Arg	Asp	Ser	Gly	Met	Asp															
		35					40					45																		
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu															
	50					55					60																			
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala															
	65				70					75					80															
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly															
				85					90					95																
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr															
		100						105					110																	
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu															
		115					120					125																		
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys															
		130				135					140																			
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu															
	145				150					155					160															
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln															
				165					170					175																
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg															
		180						185					190																	
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg															
		195					200					205																		
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp															
	210					215					220																			
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg															
	225				230					235					240															
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser															
				245					250					255																
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu															
		260						265					270																	
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn															
		275					280					285																		
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu															
	290					295					300																			
Pro	Ala	Asp	Leu	Leu	Asp	Ser																								
	305				310																									

&lt;210&gt; 801

&lt;211&gt; 1263

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1240)

&lt;223&gt; RXA00884

&lt;400&gt; 801

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catcttccgt ttcataccct gcactctacc ctgttcttag gaattcgcta tgtttaacat 60

caattaatca tgtatagggg gcaggcacta ggcttggggc atg tca gtt ttt ggt 115
                                         Met Ser Val Phe Gly
                                         1 5

gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163
Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg Cys Gly Tyr Cys Asp
                        10 15 20

ttc aac acc tat act gct ggg gaa tta ggt agt act gca ggc ccg gac 211
Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp
                        25 30 35

acc tat ctt gac tcg ttg gaa gtt gag ttg gag atg gct gtg gct tcg 259
Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser
                        40 45 50

ctg gat aat cct ccg cag gcg gaa act atc ttt att ggc ggg ggt acc 307
Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr
                        55 60 65

ccg tcg ttg att ggt gcg gac ggt ttg gcc agg gtt ttg ggg gct gtg 355
Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val
                        70 75 80 85

cgc aat act ttt ggc att gcg gat ggt gcg gaa gtc acc acg gag tcc 403
Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser
                        90 95 100

aat ccg gag tct acc tcg cct gag ttt ttt gat ggc ctg cgt gag gcg 451
Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp Gly Leu Arg Glu Ala
                        105 110 115

ggc tac aac agg att tcg tta ggg atg cag tcg gcg tcg tca agc gtt 499
Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Ser Val
                        120 125 130

ttg aag gtg ctg gac cgc acg cac acc cca ggg cgc ccg gtg gcg gcg 547
Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala
                        135 140 145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595
Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His Val Asn Leu Asp Met
                        150 155 160 165

att tat ggc acg ccg aca gag acc gat gat gat gtc cgc aag acg ctg 643
Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp Val Arg Lys Thr Leu
                        170 175 180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691
Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu
                        185 190 195

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atc gtg aaa gat ggc acg gcg atg gcg cgc aag gtg cac aag ggc gag 739
Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys Val His Lys Gly Glu
      200                      205                      210

ctg cca gcg ccg gac gag gat gtc tac gct gat cgt ttt gag ctt atc 787
Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp Arg Phe Glu Leu Ile
      215                      220                      225

gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835
Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn
      230                      235                      240                      245

tgg gcg aaa ccc ggc gga gaa tgc aag cac aac atg ggc tat tgg gtc 883
Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn Met Gly Tyr Trp Val
      250                      255                      260

gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc 931
Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly
      265                      270                      275

gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag 979
Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln
      280                      285                      290

att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg
1027
Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala
      295                      300                      305

gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa .caa
1075
Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln
      310                      315                      320                      325

ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac
1123
Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp
      330                      335                      340

cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg
1171
Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu
      345                      350                      355

gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac
1219
Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp
      360                      365                      370

att ttg ctt agt gaa gaa gac taaatattta gtaggggttac aga
1263
Ile Leu Leu Ser Glu Glu Asp
      375                      380

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&lt;210&gt; 802

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 802

Met Ser Val Phe Gly Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg  
 1 5 10 15  
 Cys Gly Tyr Cys Asp Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser  
 20 25 30  
 Thr Ala Gly Pro Asp Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu  
 35 40 45  
 Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe  
 50 55 60  
 Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg  
 65 70 75 80  
 Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu  
 85 90 95  
 Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp  
 100 105 110  
 Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser  
 115 120 125  
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly  
 130 135 140  
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His  
 145 150 155 160  
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp  
 165 170 175  
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val  
 180 185 190  
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys  
 195 200 205  
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp  
 210 215 220  
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp  
 225 230 235 240  
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn  
 245 250 255  
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala  
 260 265 270  
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala  
 275 280 285  
 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr  
 290 295 300  
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly  
 305 310 315 320  
 Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala

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          325          330          335
Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn
          340          345          350

Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp
          355          360          365

Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp
          370          375          380

<210> 803
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN02503

<400> 803
gcagcaccgg caaccacgtc cgtaacgcgc tcagaactgc cggatgcggg tatcgctcgca 60

ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115
                                         Met Thr Leu Lys Ile
                                         1           5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
          10          15          20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
          25          30          35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
          40          45          50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
          55          60          65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
          70          75          80          85

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403
Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile
          90          95          100

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451
Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly
          105          110          115

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499
Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro
          120          125          130

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tgacctggag attctccac tgc

522

&lt;210&gt; 804

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 804

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln  
 1 5 10 15

Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu  
 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu  
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His  
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr  
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Ser  
 85 90 95

Arg Glu Ala Leu Ile Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro  
 100 105 110

Glu Arg Arg Lys Gly Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala  
 115 120 125

Gln Gly Asn Pro Pro  
 130

&lt;210&gt; 805

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(535)

&lt;223&gt; FRXA02503

&lt;400&gt; 805

gcagcaccgg caaccacgtc cgtcaacgcg tcagaactgc cggatgcggg tatcgtcgca 60

ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115  
 Met Thr Leu Lys Ile  
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163  
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg  
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211  
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr  
 25 30 35



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acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
      40                      45                      50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
      55                      60                      65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
      70                      75                      80                      85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
      90                      95                      100

cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
      105                      110                      115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
      120                      125                      130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
      135                      140                      145

atgggcaagg tca 558

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&lt;210&gt; 806

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 806

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Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln
 1                      5                      10                      15

Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
      20                      25                      30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
      35                      40                      45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
      50                      55                      60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
      65                      70                      75                      80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
      85                      90                      95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
      100                      105                      110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
      115                      120                      125

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Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys  
 130 135 140

His  
 145

<210> 807  
 <211> 1245  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1222)  
 <223> RXA00377

<400> 807  
 aatggcgctc gggcagggcg cgcaagtact aaccagcaat tcccaagccc aaaaaccct 60  
 cccatatagt tcttttttact gatgcattgt cctcaattag gtg tgg ctt ctt ttc 115  
 Val Trp Leu Leu Phe  
 1 5  
 cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163  
 Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr  
 10 15 20  
 att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc 211  
 Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala  
 25 30 35  
 gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259  
 Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln  
 40 45 50  
 gcg ggt agg tcg ttg cct gag tac aag aag gtc cgt gag gga atc agc 307  
 Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser  
 55 60 65  
 atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg 355  
 Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu  
 70 75 80 85  
 cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac 403  
 Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp  
 90 95 100  
 att gtg gtg ccg ttg cgt gct gcg ggt gtt ggt gtg gaa atc gtg gcg 451  
 Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala  
 105 110 115  
 ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499  
 Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val  
 120 125 130  
 ttg aat ctt cct att ttg gag ggc aac gtt ccg gag gtg gag cag ggt 547  
 Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly  
 135 140 145

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att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt      595
Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly
150                      155                      160                      165

ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt      643
Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly
170                      175                      180

cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct      691
Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro
185                      190                      195

gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat      739
Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn
200                      205                      210

tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt      787
Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe
215                      220                      225

gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg      835
Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val
230                      235                      240                      245

ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg      883
Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu
250                      255                      260

cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg      931
Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met
265                      270                      275

agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg      979
Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu
280                      285                      290

gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg
1027
Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu
295                      300                      305

cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg
1075
Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu
310                      315                      320                      325

act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat
1123
Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp
330                      335                      340

gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt
1171
Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu
345                      350                      355

cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat
1219
Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His
360                      365                      370

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tct taaactaaga ggagtttcat gcg  
 1245  
 Ser

<210> 808  
 <211> 374  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 808  
 Val Trp Leu Leu Phe Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg  
   1                  5                  10                  15  
 Met Ser Ala Leu Thr Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala  
                   20                  25                  30  
 Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val  
           35                  40                  45  
 Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val  
   50                  55                  60  
 Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu  
   65                  70                  75                  80  
 Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala  
                   85                  90                  95  
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly  
           100                  105                  110  
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg  
   115                  120                  125  
 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro  
   130                  135                  140  
 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser  
   145                  150                  155                  160  
 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr  
           165                  170                  175  
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met  
           180                  185                  190  
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val  
   195                  200                  205  
 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp  
   210                  215                  220  
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp  
   225                  230                  235                  240  
 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val  
           245                  250                  255  
 Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu

260	265	270
Leu Leu Gly Ala Met Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp		
275	280	285
Trp Arg Val Pro Leu Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser		
290	295	300
Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala		
305	310	315
Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala		
325	330	335
Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu		
340	345	350
Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala		
355	360	365
Val Ser Ile Ile His Ser		
370		

&lt;210&gt; 809

&lt;211&gt; 681

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(658)

&lt;223&gt; RXN02504

&lt;400&gt; 809

cctcgattcc acctggctgt gccaaactcgt gcggactcgc gcgaggccct tatcgccgc 60

gacggcctga ctctggctga gcttccagaa aggcgcaaag	gtg gga act tcc gct	115
	Val Gly Thr Ser Ala	
	1 5	

cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att	163
Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile	
10 15 20	

ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc	211
Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser	
25 30 35	

ggg gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc	259
Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val	
40 45 50	

ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg	307
Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met	
55 60 65	

ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac	355
Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp	
70 75 80 85	

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403  
 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe  
                     90                    95                    100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451  
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly  
                     105                    110                    115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499  
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly  
                     120                    125                    130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547  
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp  
                     135                    140                    145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595  
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu  
                     150                    155                    160                    165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643  
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu  
                     170                    175                    180

ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681  
 Leu Gly Asp Arg Ser  
                     185

&lt;210&gt; 810

&lt;211&gt; 186

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg  
   1                    5                    10                    15

Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met  
                     20                    25                    30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala  
                     35                    40                    45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp  
                     50                    55                    60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu  
                     65                    70                    75                    80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met  
                     85                    90                    95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn  
                     100                    105                    110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu  
                     115                    120                    125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala  
                     130                    135                    140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala  
 145 150 155 160

Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala  
 165 170 175

Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser  
 180 185

<210> 811

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA02504

<400> 811

gcatctccca gctcaaggca atccgccctg acctggagat tctccactt gcgcggaaac 60

attgacaccg gcatgggcaa ggtcacctcc ggtgaactcg atg ctt gtg atg ctc 115  
 Met Leu Val Met Leu  
 1 5

gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa 163  
 Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu  
 10 15 20

gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt 211  
 Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu  
 25 30 35

gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259  
 Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn  
 40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307  
 Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr  
 55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355  
 Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His  
 70 75 80 85

gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc 403  
 Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly  
 90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451  
 Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly  
 105 110 115

gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt 499  
 Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu  
 120 125 130

atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc 548

Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser  
 135 140 145

ccgaaatttc cat

561

<210> 812

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

Met Leu Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln  
 1 5 10 15

Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro  
 20 25 30

Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr  
 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala  
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala  
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met  
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val  
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu  
 115 120 125

Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp  
 130 135 140

Arg Ser  
 145

<210> 813

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1426)

<223> RXN01162

<400> 813

catcgaatac gtgccctgct gaatagatga catcgcagag atctataaga gtcagtgggtt 60

gtcgggggttt cacagtcact tattctatgc aggattcacc atg tat atc gtg ggg 115  
 Met Tyr Ile Val Gly  
 1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163



Ile	Cys	Leu	Gln	Leu	Val	Val	Met	Ser	Gln	Pro	Met	Ser	Ala	Pro	Asp	
				10					15					20		
tcc	gct	cca	gga	aca	gag	cgc	ggt	cat	gaa	cgc	acc	cat	ttt	gcg	gta	211
Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	Thr	His	Phe	Ala	Val	
			25					30					35			
gtc	ggt	gac	tcc	cag	gat	cca	gca	cag	gca	aca	gct	cct	aga	gcg	cca	259
Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Pro	
		40					45					50				
gca	gaa	tca	att	act	ttg	att	ggt	att	ggt	acc	gat	ggg	ttt	gag	ggg	307
Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	Asp	Gly	Phe	Glu	Gly	
	55					60					65					
ctc	gga	ctc	aag	gca	cag	caa	gca	tta	caa	cgt	gcc	tct	gtg	gtg	att	355
Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	Ala	Ser	Val	Val	Ile	
	70				75					80					85	
gga	tca	tgg	cgc	cag	ctc	aat	ctc	gta	cct	gat	gcc	att	aag	gca	gag	403
Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	Ala	Ile	Lys	Ala	Glu	
				90					95					100		
cgt	cgc	cca	tgg	ccg	ggt	aat	acc	aag	cat	cct	gat	tta	gat	gcc	ttg	451
Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	Asp	Leu	Asp	Ala	Leu	
			105					110					115			
ttt	aaa	gag	ttc	ctc	ggt	cgg	cat	gtt	gct	gtt	ctg	gcc	tct	ggc	gat	499
Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	Leu	Ala	Ser	Gly	Asp	
	120						125					130				
cca	ctg	ttt	tac	ggc	gtg	ggc	acc	gca	atg	gtc	cat	gtg	ctg	ggg	atg	547
Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	His	Val	Leu	Gly	Met	
	135					140					145					
gat	aga	ctc	acg	gtt	att	ccg	gga	cca	tca	tcc	gcg	tcg	ctt	gct	tgc	595
Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	Ala	Ser	Leu	Ala	Cys	
	150				155					160					165	
gcc	cgc	ttg	ggt	tgg	aca	gtc	aac	cgc	aca	cgg	gtg	gtg	tac	cta	gga	643
Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	Val	Val	Tyr	Leu	Gly	
				170					175					180		
caa	gaa	ccc	att	gag	aca	ctc	atc	ccg	att	att	gaa	tca	ggc	gct	caa	691
Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	Glu	Ser	Gly	Ala	Gln	
			185					190					195			
ttc	ctc	gtc	ttg	ggt	aaa	gat	gaa	ttc	agt	aca	gct	caa	gtt	gcc	acg	739
Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	Ala	Gln	Val	Ala	Thr	
		200					205					210				
ttg	ttg	aat	gaa	ctc	gga	ctg	ggg	gag	act	cca	ctg	act	gtg	ctc	agc	787
Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	Leu	Thr	Val	Leu	Ser	
	215					220					225					
gat	ttg	ggc	agt	act	gat	gag	gag	atc	acc	caa	ggc	aca	gct	tca	cat	835
Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	Gly	Thr	Ala	Ser	His	
	230				235					240				245		
cca	cca	gct	gca	gtg	tct	gtt	ctc	aac	gtg	att	gct	gtg	gga	gct	cgc	883
Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	Ala	Val	Gly	Ala	Arg	

	250		255		260	
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac						931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp						
	265		270		275	
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg						979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met						
	280		285		290	
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta						
1027						
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu						
	295		300		305	
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt						
1075						
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val						
	310		315		320	325
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt						
1123						
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser						
	330		335		340	
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta						
1171						
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val						
	345		350		355	
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc						
1219						
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly						
	360		365		370	
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct						
1267						
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro						
	375		380		385	
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag						
1315						
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys						
	390		395		400	405
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc						
1363						
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg						
	410		415		420	
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act						
1411						
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr						
	425		430		435	
cca gaa gcg gtg aat tagcatcaaa aaccaacccc atg						
1449						
Pro Glu Ala Val Asn						
	440					

<210> 814  
 <211> 442  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 814

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Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
 1           5           10           15

Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
          20           25           30

Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
          35           40           45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
          50           55           60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65           70           75           80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
          85           90           95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
          100          105          110

Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
          115          120          125

Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
          130          135          140

His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
          145          150          155          160

Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
          165          170          175

Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
          180          185          190

Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
          195          200          205

Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
          210          215          220

Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
          225          230          235          240

Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
          245          250          255

Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
          260          265          270

Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
          275          280          285

Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu

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290	295	300
Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser 305 310 315 320		
Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly 325 330 335		
Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys 340 345 350		
Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile 355 360 365		
Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp 370 375 380		
Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu 385 390 395 400		
Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile 405 410 415		
Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val 420 425 430		
Thr Lys Pro Val Thr Pro Glu Ala Val Asn 435 440		

&lt;210&gt; 815

&lt;211&gt; 1345

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; FRXA01162

&lt;400&gt; 815

catcgaatac gtgccctgct gaatagatga catcgcagag atctataaga gtcagtgggt 60

gtcgggggttt cacagtcact tattctatgc aggattcacc	atg tat atc gtg ggg	115
	Met Tyr Ile Val Gly	
	1 5	

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac	163
Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp	
10 15 20	

tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta	211
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val	
25 30 35	

gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca	259
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro	
40 45 50	

gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg	307
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly	

55	60	65	
ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att			355
Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile			
70	75	80	85
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag			403
Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu			
	90	95	100
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg			451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu			
	105	110	115
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat			499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp			
	120	125	130
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg			547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met			
	135	140	145
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc			595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys			
	150	155	160
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga			643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly			
	170	175	180
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa			691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln			
	185	190	195
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg			739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr			
	200	205	210
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc			787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser			
	215	220	225
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat			835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His			
	230	235	240
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc			883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg			
	250	255	260
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
	265	270	275
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
	280	285	290
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			
1027			
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

295 300 305  
 cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt  
 1075  
 Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val  
 310 315 320 325  
 gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt  
 1123  
 Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser  
 330 335 340  
 gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta  
 1171  
 Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val  
 345 350 355  
 caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc  
 1219  
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly  
 360 365 370  
 cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct  
 1267  
 Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro  
 375 380 385  
 gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag  
 1315  
 Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys  
 390 395 400 405  
 ctt cac aca ctc caa gaa caa cac ggc gga  
 1345  
 Leu His Thr Leu Gln Glu Gln His Gly Gly  
 410 415  
  
 <210> 816  
 <211> 415  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 816  
 Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro  
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 Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg  
 20 25 30  
 Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr  
 35 40 45  
 Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr  
 50 55 60  
 Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg  
 65 70 75 80  
 Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp  
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro  
 100 105 110  
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val  
 115 120 125  
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val  
 130 135 140  
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser  
 145 150 155 160  
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg  
 165 170 175  
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile  
 180 185 190  
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr  
 195 200 205  
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro  
 210 215 220  
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln  
 225 230 235 240  
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile  
 245 250 255  
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp  
 260 265 270  
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro  
 275 280 285  
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu  
 290 295 300  
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser  
 305 310 315 320  
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly  
 325 330 335  
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys  
 340 345 350  
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile  
 355 360 365  
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp  
 370 375 380  
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu  
 385 390 395 400  
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly  
 405 410 415





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atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac 691
Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp
      185                      190                      195

ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739
Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr
      200                      205                      210

act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787
Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala
      215                      220                      225

gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835
Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly
      230                      235                      240                      245

caa gtt gct ggc ctc taagcagatc gcctaagaat ggg 873
Gln Val Ala Gly Leu
      250

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<210> 818
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

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<400> 818
Met Thr Ile Ser Gln Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu
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Ile Gly Gly Gly Pro Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met
      20           25           30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro
      35           40           45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val
      50           55           60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr
      65           70           75           80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg
      85           90           95

Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu
      100          105          110

Glu Phe Leu Gly Glu His Gly Ile Glu Cys Glu Val Ile Pro Gly Val
      115          120          125

Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn
      130          135          140

Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro
      145          150          155          160

Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly
      165          170          175

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Gly	Thr	Leu	Ser	Ile	Ile	Met	Gly	Val	Lys	Asn	Ala	Gly	Ala	Ile	Ala
			180					185					190		
Gln	Ala	Leu	Met	Asp	Gly	Gly	Leu	Asp	Ala	Asp	Thr	Pro	Ala	Ala	Val
		195					200					205			
Ile	Gln	Glu	Gly	Thr	Thr	Asp	Ala	Gln	Arg	Ser	Val	Arg	Cys	Thr	Leu
	210					215					220				
Gly	Thr	Leu	Gly	Ala	Val	Met	Val	Glu	Glu	Glu	Ile	Lys	Pro	Pro	Ala
225					230					235					240
Val	Tyr	Val	Ile	Gly	Gln	Val	Ala	Gly	Leu						
				245					250						

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<210> 819
<211> 1917
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1894)  
<223> RXN00371
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acgttgggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115																
Met Thr Ile Ala His 5																
aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163																
Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser 20																
gaa acc atc ggg gtt gaa tcg ctg acg cac gga aac tta cgt cct gtt 211																
Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val 35																
tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259																
Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro 50																
ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307																
Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu 65																
aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355																
Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr 85																
gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403																
Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile 100																
cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451																
Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg 115																

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atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt 499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg
120 125 130

cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act 547
Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr
135 140 145

cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga 595
Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly
150 155 160 165

gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca 643
Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr
170 175 180

ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg 691
Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val
185 190 195

gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att 739
Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile
200 205 210

gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg 787
Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu
215 220 225

gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc 835
Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala
230 235 240 245

cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat 883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn
250 255 260

atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt 931
Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg
265 270 275

ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat 979
Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp
280 285 290

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg gat
1027
Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp
295 300 305

gat cgc tcc aag tac tct tgg tgg gaa aac cgc gct ctg tac ggt tgg
1075
Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp
310 315 320 325

cgt gtg ctg gtg cct cgc gct cgg gag caa gcg gca tcc atg tcc gca
1123
Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala
330 335 340

cgt ctg agc agc cac ggc gct atc ccg cag gaa gtc cct acc att tct
1171

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Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser  
 345 350 355  
 gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc atc aag ggc  
 1219  
 Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly  
 360 365 370  
 atc gtc gaa gga cgc tac cag tgg gtt gtc ctc acc agc gtc aac gca  
 1267  
 Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala  
 375 380 385  
 gtg aag gca gtc tgg gag aaa atc acc gaa ttc ggc ctc gat tca cgt  
 1315  
 Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe Gly Leu Asp Ser Arg  
 390 395 400 405  
 tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa acc gcc gct  
 1363  
 Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala  
 410 415 420  
 gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct gca cgt acc  
 1411  
 Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro Ala Arg Thr  
 425 430 435  
 agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa tat ttc gaa  
 1459  
 Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu  
 440 445 450  
 gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca gat atc gca  
 1507  
 Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala  
 455 460 465  
 acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg gaa gtc gaa  
 1555  
 Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp Glu Val Glu  
 470 475 480 485  
 gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca agc gct gat  
 1603  
 Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro Ser Ala Asp  
 490 495 500  
 atc cga gat atg atc aag acc ggc gga ttt gat gca gtt gcc ttc acc  
 1651  
 Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val Ala Phe Thr  
 505 510 515  
 tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt aaa cca cac  
 1699  
 Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His  
 520 525 530  
 cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca gcg acc gct  
 1747  
 Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala

535 540 545

gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc gcc gaa gta  
1795

Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile Ala Glu Val  
550 555 560 565

cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat ctg cgc gct  
1843

Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp Leu Arg Ala  
570 575 580

aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt cga aaa gcg  
1891

Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg Arg Lys Ala  
585 590 595

tct taaaaggttt ttcactaggg tgt  
1917  
Ser

<210> 820  
<211> 598  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 820

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu  
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Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly  
20 25 30

Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr  
35 40 45

Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly  
50 55 60

Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala  
65 70 75 80

Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe  
85 90 95

Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu  
100 105 110

Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg  
115 120 125

Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu  
130 135 140

Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala  
145 150 155 160

Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu  
165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly  
 180 185 190  
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro  
 195 200 205  
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val  
 210 215 220  
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro  
 225 230 235 240  
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu  
 245 250 255  
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala  
 260 265 270  
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu  
 275 280 285  
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu  
 290 295 300  
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg  
 305 310 315 320  
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala  
 325 330 335  
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu  
 340 345 350  
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu  
 355 360 365  
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu  
 370 375 380  
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe  
 385 390 395 400  
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly  
 405 410 415  
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu  
 420 425 430  
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe  
 435 440 445  
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro  
 450 455 460  
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu  
 465 470 475 480  
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala  
 485 490 495

Pro Pro. Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp  
                   500                                  505                                  510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile  
                   515                                  520                                  525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met  
                   530                                  535                                  540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro  
                   545                                  550                                  555                                  560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val  
                                   565                                  570                                  575

Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg  
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Arg Arg Arg Lys Ala Ser  
                   595

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1024)  
 <223> FRXA00371

<400> 821  
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acgttggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115  
   Met Thr Ile Ala His  
   1                                  5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163  
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser  
                                   10                                  15                                  20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211  
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val  
                                   25                                  30                                  35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259  
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro  
                   40                                  45                                  50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307  
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu  
                   55                                  60                                  65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355  
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr  
                   70                                  75                                  80                                  85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403  
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile

	90	95	100	
cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc				451
Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg				
	105	110	115	
atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt				499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg				
	120	125	130	
cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act				547
Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr				
	135	140	145	
cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga				595
Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly				
	150	155	160	165
gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca				643
Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr				
	170	175	180	
ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg				691
Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val				
	185	190	195	
gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att				739
Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile				
	200	205	210	
gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg				787
Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu				
	215	220	225	
gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc				835
Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala				
	230	235	240	245
cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat				883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn				
	250	255	260	
atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt				931
Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg				
	265	270	275	
ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat				979
Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp				
	280	285	290	
gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg				
1024				
Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val				
	295	300	305	

&lt;210&gt; 822

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 822

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Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
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Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
      20              25              30

Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
      35              40              45

Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50              55              60

Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65              70              75              80

Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
      85              90              95

Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
      100              105              110

Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
      115              120              125

Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
      130              135              140

Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
      145              150              155              160

Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
      165              170              175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
      180              185              190

Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
      195              200              205

Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
      210              215              220

Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
      225              230              235              240

Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
      245              250              255

Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
      260              265              270

Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
      275              280              285

Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
      290              295              300

Gly Lys Gly Val
      305

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 <211> 755  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(732)  
 <223> FRXA00374

<400> 823  
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 atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc 96  
 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser  
 20 25 30  
 gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc 144  
 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu  
 35 40 45  
 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192  
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys  
 50 55 60  
 acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct 240  
 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro  
 65 70 75 80  
 gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa 288  
 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu  
 85 90 95  
 tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca 336  
 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala  
 100 105 110  
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384  
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp  
 115 120 125  
 gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca 432  
 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro  
 130 135 140  
 agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt 480  
 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val  
 145 150 155 160  
 gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt 528  
 Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly  
 165 170 175  
 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576  
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala  
 180 185 190  
 gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc 624

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile  
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672  
 Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp  
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720  
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg  
 225 230 235 240

cga aaa gcg tct taaaagggttt ttcactaggg tgt 755  
 Arg Lys Ala Ser

&lt;210&gt; 824

&lt;211&gt; 244

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 824

Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala  
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Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser  
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu  
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys  
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro  
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu  
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala  
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp  
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro  
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val  
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly  
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala  
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile  
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp  
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg  
 225 230 235 240

Arg Lys Ala Ser

<210> 825

<211> 1467

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1444)

<223> RXN00383

<400> 825

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agccgtctcc atcattcatt cttaactaa gaggagtttc atg cgt ttt gcc atc 115  
 Met Arg Phe Ala Ile  
 1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163  
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys  
 10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211  
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile  
 25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259  
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile  
 40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307  
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe  
 55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355  
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys  
 70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403  
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly  
 90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451  
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala  
 105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499  
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg  
 120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547  
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu

135	140	145	
ggt ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc			595
Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser			
150	155	160	165
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag			643
Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu			
	170	175	180
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa			691
Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu			
	185	190	195
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag			739
Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys			
	200	205	210
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca			787
Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala			
	215	220	225
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa			835
Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu			
	230	235	240
ggt ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att			883
Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile			
	250	255	260
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca			931
Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala			
	265	270	275
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca			979
Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala			
	280	285	290
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc			
1027			
Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser			
	295	300	305
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc			
1075			
Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe			
	310	315	320
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg			
1123			
Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala			
	330	335	340
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc			
1171			
Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg			
	345	350	355
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc			
1219			
Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr			

360                      365                      370  
 ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg  
 1267  
 Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val  
       375                      380                      385  
 cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct  
 1315  
 Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala  
 390                      395                      400                      405  
 acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa  
 1363  
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu  
                     410                      415                      420  
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca  
 1411  
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala  
                     425                      430                      435  
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat  
 1464  
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly  
       440                      445  
 tga  
 1467  
  
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 <211> 448  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 826  
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 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu  
                     20                      25                      30  
 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser  
                     35                      40                      45  
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp  
                     50                      55                      60  
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser  
                     65                      70                      75                      80  
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala  
                     85                      90                      95  
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly  
                     100                      105                      110  
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val  
                     115                      120                      125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val  
 130 135 140  
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu  
 145 150 155 160  
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu  
 165 170 175  
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val  
 180 185 190  
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val  
 195 200 205  
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala  
 210 215 220  
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile  
 225 230 235 240  
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr  
 245 250 255  
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu  
 260 265 270  
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys  
 275 280 285  
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly  
 290 295 300  
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile  
 305 310 315 320  
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu  
 325 330 335  
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp  
 340 345 350  
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu  
 355 360 365  
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu  
 370 375 380  
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly  
 385 390 395 400  
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala  
 405 410 415  
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val  
 420 425 430  
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly  
 435 440 445

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<210> 827
<211> 382
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(382)  
<223> FRXA00376
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<400> 827																		
ccat	atc	tctt	aac	ctt	gggc	atg	gtg	tgct	tcct	aat	acg	gtg	gcg	gaag	atatt	actga	60	
agcc	gtct	cc	atc	att	catt	ctta	aact	aa	gagg	agtttc	atg	cgt	ttt	gcc	atc		115	
											Met	Arg	Phe	Ala	Ile			
											1				5			
atc	ggt	gca	ggc	ctt	gcg	ggt	ctg	act	gct	gca	tat	gag	atc	cat	aaa		163	
Ile	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Thr	Ala	Ala	Tyr	Glu	Ile	His	Lys			
				10					15					20				
gct	gat	ccc	act	gcc	caa	atc	gat	gtg	ttg	gaa	gca	ggc	gaa	cgc	att		211	
Ala	Asp	Pro	Thr	Ala	Gln	Ile	Asp	Val	Leu	Glu	Ala	Gly	Glu	Arg	Ile			
				25					30					35				
ggc	ggc	aag	ctt	ttt	acg	gtg	ccg	ttt	gct	tcc	gga	cct	acc	gat	att		259	
Gly	Gly	Lys	Leu	Phe	Thr	Val	Pro	Phe	Ala	Ser	Gly	Pro	Thr	Asp	Ile			
			40					45					50					
gga	gcg	gag	gcg	ttt	tta	gct	gcg	cgt	tcc	gat	gcg	gtg	gag	ttt	ttt		307	
Gly	Ala	Glu	Ala	Phe	Leu	Ala	Ala	Arg	Ser	Asp	Ala	Val	Glu	Phe	Phe			
			55					60					65					
act	gag	ctt	ggg	ttg	gct	gat	tct	ttg	gtc	agc	ccg	tct	gct	gcg	aag		355	
Thr	Glu	Leu	Gly	Leu	Ala	Asp	Ser	Leu	Val	Ser	Pro	Ser	Ala	Ala	Lys			
		70					75					80					85	
tct	cag	tat	ttc	gcg	ggc	ggt	gcg	ctg										382
Ser	Gln	Tyr	Phe	Ala	Gly	Gly	Ala	Leu										
				90														

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<210> 828
<211> 94
<212> PRT
<213> Corynebacterium glutamicum
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<400> 828

Met	Arg	Phe	Ala	Ile	Ile	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Thr	Ala	Ala
1				5					10					15	
Tyr	Glu	Ile	His	Lys	Ala	Asp	Pro	Thr	Ala	Gln	Ile	Asp	Val	Leu	Glu
			20					25					30		
Ala	Gly	Glu	Arg	Ile	Gly	Gly	Lys	Leu	Phe	Thr	Val	Pro	Phe	Ala	Ser
		35					40					45			
Gly	Pro	Thr	Asp	Ile	Gly	Ala	Glu	Ala	Phe	Leu	Ala	Ala	Arg	Ser	Asp



50	55	60	
Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser			
65	70	75	80
Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu			
	85	90	
 <210> 829			
<211> 1037			
<212> DNA			
<213> Corynebacterium glutamicum			
 <220>			
<221> CDS			
<222> (1)..(1014)			
<223> FRXA00383			
 <400> 829			
gca ggc gcg caa gac acc gct ttt gat tgg act cct ggc caa gac att			48
Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile			
1	5	10	15
tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat			96
Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp			
	20	25	30
act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat			144
Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp			
	35	40	45
gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat			192
Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp			
	50	55	60
cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag			240
Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys			
65	70	75	80
gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc			288
Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg			
	85	90	95
ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg			336
Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala			
	100	105	110
ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc			384
Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser			
	115	120	125
gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt gcc gaa			432
Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu			
	130	135	140
ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct			480
Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala			
145	150	155	160
gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca			528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala  
 165 170 175  
 att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576  
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser  
 180 185 190  
 gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624  
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro  
 195 200 205  
 ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672  
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His  
 210 215 220  
 ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720  
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu  
 225 230 235 240  
 ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768  
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala  
 245 250 255  
 gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816  
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala  
 260 265 270  
 gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864  
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala  
 275 280 285  
 tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912  
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile  
 290 295 300  
 gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960  
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val  
 305 310 315 320  
 gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg  
 1008  
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu  
 325 330 335  
 ctg gga taagcaccca aaaacactat tga  
 1037  
 Leu Gly

&lt;210&gt; 830

&lt;211&gt; 338

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 830

Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile  
 1 5 10 15

Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp  
 20 25 30

Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp  
 35 40 45  
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp  
 50 55 60  
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys  
 65 70 75 80  
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg  
 85 90 95  
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala  
 100 105 110  
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser  
 115 120 125  
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu  
 130 135 140  
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala  
 145 150 155 160  
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Pro His Leu Arg Ala  
 165 170 175  
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser  
 180 185 190  
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro  
 195 200 205  
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His  
 210 215 220  
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu  
 225 230 235 240  
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala  
 245 250 255  
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala  
 260 265 270  
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala  
 275 280 285  
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile  
 290 295 300  
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val  
 305 310 315 320  
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu  
 325 330 335  
 Leu Gly

<210> 831  
 <211> 873  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(850)  
 <223> RXA01253

<400> 831  
 acgccatcgc agcctgccct cctggccgca tcgaagtcct cgccaactac accgcattcc 60  
 gagacctcaa aaaggctctg gagaaagggg ccgaacaata atg acc acc ctc aac 115  
 Met Thr Thr Leu Asn  
 1 5  
 atc ggc ctc atc ctc ccc gac gtc ctc gga act tac ggc gac gac ggc 163  
 Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr Tyr Gly Asp Asp Gly  
 10 15 20  
 aac gca cta gtc ctg cgc caa cgc gca cgc atg cgt ggc att aat gct 211  
 Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met Arg Gly Ile Asn Ala  
 25 30 35  
 gaa atc cag cgc gtc acc ctc gac gac gcc gtc cct tcc acc ctt gat 259  
 Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val Pro Ser Thr Leu Asp  
 40 45 50  
 ctc tac tgc ctc ggc ggc ggc gag gac acc gca cag atc ctt gcc acc 307  
 Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala Gln Ile Leu Ala Thr  
 55 60 65  
 gaa cac ctc acc aaa gac ggc ggc ctc caa acc gca gcc gcc gca ggc 355  
 Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr Ala Ala Ala Ala Gly  
 70 75 80 85  
 cgc ccc atc ttc gca gtc tgc gca ggt ctc cag gta ctc ggc gac tcc 403  
 Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln Val Leu Gly Asp Ser  
 90 95 100  
 ttc cgc gcc gcc ggc cgt gtc atc gac ggc ctt ggg ctt atc gac gcc 451  
 Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu Gly Leu Ile Asp Ala  
 105 110 115  
 acc acc gtc tct tta caa aaa cgc gcc atc gga gaa gtc gaa acg aca 499  
 Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly Glu Val Glu Thr Thr  
 120 125 130  
 cca acc cgc gcc gga ttc acc gcc gag ctg acc gaa cga ctc acc ggc 547  
 Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr Glu Arg Leu Thr Gly  
 135 140 145  
 ttc gaa aac cac atg ggc gcc acc ctg ctc ggc ccc gac gcc gaa cca 595  
 Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly Pro Asp Ala Glu Pro  
 150 155 160 165  
 ctc ggc cga gtc gtc cgc ggc gaa ggc aac acc gat gtc tgg gca gcc 643  
 Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr Asp Val Trp Ala Ala  
 170 175 180

tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691  
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val  
 185 190 195  
 caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739  
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg  
 200 205 210  
 aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787  
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala  
 215 220 225  
 ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835  
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg  
 230 235 240 245  
 gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta 873  
 Ala Glu Arg Leu Ala  
 250

&lt;210&gt; 832

&lt;211&gt; 250

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr  
 1 5 10 15  
 Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met  
 20 25 30  
 Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val  
 35 40 45  
 Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala  
 50 55 60  
 Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr  
 65 70 75 80  
 Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln  
 85 90 95  
 Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu  
 100 105 110  
 Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly  
 115 120 125  
 Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr  
 130 135 140  
 Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly  
 145 150 155 160  
 Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr  
 165 170 175

Asp	Val	Trp	Ala	Ala	Ser	Glu	Asn	Thr	Asp	Asp	Gln	Arg	Gln	Gln	Phe
			180					185					190		
Ala	Glu	Gly	Ala	Val	Gln	Gly	Ser	Ile	Ile	Ala	Thr	Tyr	Met	His	Gly
		195					200					205			
Pro	Ala	Leu	Ala	Arg	Asn	Pro	Gln	Leu	Ala	Asp	Leu	Met	Leu	Ala	Lys
	210					215					220				
Ala	Met	Gly	Val	Ala	Leu	Lys	Asp	Leu	Glu	Pro	Leu	Asp	Ile	Asp	Val
225					230					235					240
Ile	Asp	Arg	Leu	Arg	Ala	Glu	Arg	Leu	Ala						
			245						250						

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<210> 833
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1021)  
<223> RXA02134
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<400> 833																
tgatgaacga	catgtcgaca	ttttcttcg	ccggcgtcga	tgaccacctta	aacgcctctt	60										
ccgaagcgcc	cgagcaaaac	acggagtaac	tttctaagcg	atg	tcc	ggc	aaa	gca	115							
				Met	Ser	Gly	Lys	Ala								
				1				5								
ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac	163															
Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn																
	10							15						20		
ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc	211															
Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu																
	25						30						35			
ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta	259															
Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val																
	40					45				50						
atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg	307															
Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala																
	55					60				65						
atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat	355															
Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp																
	70				75				80					85		
gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat	403															
Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn																
	90							95					100			
cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt	451															
Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly																
	105						110					115				

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tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499
Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg
      120                125                130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547
Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln
      135                140                145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595
Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile
      150                155                160                165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643
Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu
      170                175                180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691
Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
      185                190                195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
      200                205                210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
      215                220                225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
      230                235                240                245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
      250                255                260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
      265                270                275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
      280                285                290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg
1021
Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
      295                300                305

taaagcgggtg gcgtcttttg gga
1044

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&lt;210&gt; 834

&lt;211&gt; 307

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 834

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Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp
  1              5              10              15

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Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn  
                   20                  25                  30  
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr  
                   35                  40                  45  
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe  
                   50                  55                  60  
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly  
                   65                  70                  75                  80  
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe  
                   85                  90                  95  
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val  
                   100                  105                  110  
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile  
                   115                  120                  125  
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu  
                   130                  135                  140  
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr  
                   145                  150                  155                  160  
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly  
                   165                  170                  175  
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe  
                   180                  185                  190  
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp  
                   195                  200                  205  
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser  
                   210                  215                  220  
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro  
                   225                  230                  235                  240  
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile  
                   245                  250                  255  
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu  
                   260                  265                  270  
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile  
                   275                  280                  285  
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn  
                   290                  295                  300  
 Ala Met Val  
 305

&lt;210&gt; 835

&lt;211&gt; 1197



&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1174)

&lt;223&gt; RXA02135

&lt;400&gt; 835

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aaaacgtttt	aagaaaacag	tcgggttgaa	ggagttgtta	atg	ggt	cca	gca	gag	115
				Met	Val	Pro	Ala	Glu	
				1				5	

ctt	ttt	gcg	cgt	gtg	gaa	ttt	ccg	gat	cat	aaa	atc	ctg	gct	cag	acg	163
Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys	Ile	Leu	Ala	Gln	Thr	
			10					15						20		

aag	gat	ttc	cat	gac	tcc	ctc	acc	aag	cca	ccc	gga	tct	ttg	ggc	aag	211
Lys	Asp	Phe	His	Asp	Ser	Leu	Thr	Lys	Pro	Pro	Gly	Ser	Leu	Gly	Lys	
			25					30					35			

ttg	gag	cag	atc	ggc	tgt	ttc	att	tcc	gca	tgc	cag	ggc	cag	att	ccg	259
Leu	Glu	Gln	Ile	Gly	Cys	Phe	Ile	Ser	Ala	Cys	Gln	Gly	Gln	Ile	Pro	
		40					45					50				

cca	cgt	cca	ctc	aac	aac	tca	aag	atc	ggt	ggt	ttc	gct	ggc	gat	cac	307
Pro	Arg	Pro	Leu	Asn	Asn	Ser	Lys	Ile	Val	Val	Phe	Ala	Gly	Asp	His	
	55					60					65					

ggc	ggt	gca	act	aaa	ggc	gtg	tcc	gcg	tac	cca	tcc	tca	gta	agc	ttg	355
Gly	Val	Ala	Thr	Lys	Gly	Val	Ser	Ala	Tyr	Pro	Ser	Ser	Val	Ser	Leu	
	70				75					80					85	

cag	atg	gct	gaa	aac	att	aca	aac	ggt	ggc	gcc	gcc	atc	aac	gtg	att	403
Gln	Met	Ala	Glu	Asn	Ile	Thr	Asn	Gly	Gly	Ala	Ala	Ile	Asn	Val	Ile	
				90					95					100		

gca	cgc	acc	acc	ggc	acg	tcc	gtc	cga	ctt	att	gat	acc	tcc	ctc	gac	451
Ala	Arg	Thr	Thr	Gly	Thr	Ser	Val	Arg	Leu	Ile	Asp	Thr	Ser	Leu	Asp	
			105					110					115			

cac	gaa	gca	tgg	ggc	gac	gag	cgc	gta	tct	agg	tcc	tgc	gga	tcc	atc	499
His	Glu	Ala	Trp	Gly	Asp	Glu	Arg	Val	Ser	Arg	Ser	Cys	Gly	Ser	Ile	
		120					125					130				

gat	ggt	gaa	gac	gcc	atg	acc	caa	gaa	cag	gtc	gaa	cgc	gca	ctg	aag	547
Asp	Val	Glu	Asp	Ala	Met	Thr	Gln	Glu	Gln	Val	Glu	Arg	Ala	Leu	Lys	
		135				140					145					

atc	ggt	aag	cgc	att	gcg	gat	caa	gaa	gtg	gac	gca	ggc	gcc	gac	att	595
Ile	Gly	Lys	Arg	Ile	Ala	Asp	Gln	Glu	Val	Asp	Ala	Gly	Ala	Asp	Ile	
	150				155					160				165		

tta	atc	ccc	ggc	gat	tta	gga	att	ggc	aac	acc	acc	acc	gcc	gct	gcc	643
Leu	Ile	Pro	Gly	Asp	Leu	Gly	Ile	Gly	Asn	Thr	Thr	Thr	Ala	Ala	Ala	
			170					175						180		

ctc	ggt	gga	acg	ttc	acc	ctc	gca	gag	cct	ggt	ggt	gtc	gta	ggc	cgc	691
Leu	Val	Gly	Thr	Phe	Thr	Leu	Ala	Glu	Pro	Val	Val	Val	Val	Gly	Arg	

185	190	195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc			739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile			
200	205	210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc			787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala			
215	220	225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc			835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe			
230	235	240	245
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac gcc gtt			883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val			
250	255	260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc			931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala			
265	270	275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc			979
Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser			
280	285	290	
gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg			
1027			
Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met			
295	300	305	
tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag			
1075			
Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys			
310	315	320	325
att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc gcc			
1123			
Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly			
330	335	340	
gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg			
1171			
Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr			
345	350	355	
gag taactttcta agcgatgtcc ggc			
1197			
Glu			
<210> 836			
<211> 358			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 836			
Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys			
1	5	10	15

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Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
      20                      25                      30

Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
      35                      40                      45

Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
      50                      55                      60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
      65                      70                      75                      80

Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
      85                      90                      95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
      100                     105                     110

Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
      115                     120                     125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
      130                     135                     140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
      145                     150                     155                     160

Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
      165                     170                     175

Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
      180                     185                     190

Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
      195                     200                     205

Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
      210                     215                     220

Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
      225                     230                     235                     240

Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
      245                     250                     255

Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
      260                     265                     270

Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
      275                     280                     285

Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
      290                     295                     300

Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
      305                     310                     315                     320

Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
      325                     330                     335

Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala

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340                               345                               350

Pro Glu Gln Asn Thr Glu
355

<210> 837
<211> 645
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXA02136

<400> 837
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ccctcgtgca cgcgttgaaa ttggtgctga agtctagcgc atg cgc acg tta gtt 115
Met Arg Thr Leu Val
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

```

```

150              155              160              165
ggt ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga      642
Gly Leu Pro Leu Glu Leu Lys Thr Phe
              170

```

**agg** 645

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<210> 838
<211> 174
<212> PRT
<213> Corynebacterium glutamicum
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<400> 838  
Met Arg Thr Leu Val Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe  
1 5 10 15

Ala Glu Ser Leu Val Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala  
20 25 30

Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His  
35 40 45

Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val  
50 55 60

Asp Lys Leu Leu Ala Ser Pro. Pro Ala Met Pro Val Leu Val Asp Asp  
65 70 75 80

Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu  
85 90 95

Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala  
100 105 110

Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val  
115 120 125

Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp  
130 135 140

Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val  
145 150 155 160

Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe  
165 170

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<210> 839
<211> 575
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(552)  
<223> RXN03114
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<400> 839  
act ccg ggg cat ttt gtt gcg ctc gcg cgg gag att gcg ggc gcg gtg 48

```

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1           5           10           15

cgc cgc gag ttg acg gtg ggg ttg gat gct ggt gac ggt ccg att tta 96
Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
           20           25           30

agg cag agc ttt gat gtt ggt ttt ttg ctt gtc gac gcc tcc ttc cac 144
Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His
           35           40           45

att cat atc aat ggc gtg tct act ggg cag tcg gtt gcg ccg gat gat 192
Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
           50           55           60

gta gtt gag gtg gtg cgt ggt ttg gct gat gct tcg gag ttg tcc gtg 240
Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
           65           70           75           80

gaa agt gtt gct gag ttg tgt act ccc gtg gca ccg gtt tca tta tct 288
Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
           85           90           95

gag gca cag ggg aat cct gcg cct att ggg tgg ttg gag cat gat ggc 336
Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
           100           105           110

gtg gtg tcg ttg ggt gcg ggt att cca ggg ggg cgg gtg gag gct cgt 384
Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
           115           120           125

tta gcg cgt ttt att gcg gtg att gag gcg gag acc act att acc cca 432
Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
           130           135           140

tgg aat tcg ttg atc att cat gat ttg tat gag ggt gtt gca gaa cag 480
Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
           145           150           155           160

gtg gtg aag gtt ctg gct ccc atg ggg ttg gtt ttt gat gct aat tca 528
Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
           165           170           175

ccg ctt ctg gag tca ccg gct ttg taactcgcca ttggtgcacg tct 575
Pro Leu Leu Glu Ser Pro Ala Leu
           180

```

&lt;210&gt; 840

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 840

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Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1           5           10           15

Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
           20           25           30

Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His

```

35	40	45
Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp		
50	55	60
Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val		
65	70	75 80
Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser		
	85	90 95
Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly		
	100	105 110
Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg		
	115	120 125
Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro		
	130	135 140
Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln		
145	150	155 160
Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser		
	165	170 175
Pro Leu Leu Glu Ser Pro Ala Leu		
	180	

&lt;210&gt; 841

&lt;211&gt; 1200

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1177)

&lt;223&gt; RXN01810

&lt;400&gt; 841

ccaccaccac aatgttgctc atcctcgcg cgttcggtgt cgcaggtggc tccatgactc 60

gcttcaccgt	cggaacccg	actggaaaat	aaggcttcac	atg aat aac gct ttt	115
				Met Asn Asn Ala Phe	
				1 5	

cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg	163
Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr	
	10 15 20

gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg	211
Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu	
	25 30 35

att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc	259
Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe	
	40 45 50

aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc	307
Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr	

55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc			355
Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly			
70	75	80	85
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc			403
Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu			
	90	95	100
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat			451
Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn			
	105	110	115
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att			499
Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile			
	120	125	130
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt			547
Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu			
	135	140	145
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc			595
Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg			
150	155	160	165
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg			643
Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met			
	170	175	180
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc			691
Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile			
	185	190	195
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt			739
Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg			
	200	205	210
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc			787
Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr			
	215	220	225
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt			835
Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly			
230	235	240	245
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att			883
Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile			
	250	255	260
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat			931
Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp			
	265	270	275
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc			979
Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val			
	280	285	290
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt			
1027			
Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			



295                                      300                                      305  
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa  
 1075  
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln  
 310                                      315                                      320                                      325  
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa  
 1123  
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln  
 330                                      335                                      340  
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc  
 1171  
 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly  
 345                                      350                                      355  
 ggc gag tagatggttg tgaaggaggt tga  
 1200  
 Gly Glu

<210> 842  
 <211> 359  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 842  
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 1                                      5                                      10                                      15  
 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser  
 20                                      25                                      30  
 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr  
 35                                      40                                      45  
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp  
 50                                      55                                      60  
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu  
 65                                      70                                      75                                      80  
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile  
 85                                      90                                      95  
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu  
 100                                      105                                      110  
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro  
 115                                      120                                      125  
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn  
 130                                      135                                      140  
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His  
 145                                      150                                      155                                      160  
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val  
 165                                      170                                      175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp  
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu  
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val  
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr  
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly  
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu  
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu  
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr  
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr  
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu  
 325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu  
 340 345 350

Leu Tyr Val Gln Gly Gly Glu  
 355

&lt;210&gt; 843

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(933)

&lt;223&gt; RXS03205

&lt;400&gt; 843

gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48  
 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg	
180 185 190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg	
195 200 205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp	
210 215 220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg	
225 230 235 240	
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser	
245 250 255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg	816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu	
260 265 270	
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac	864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn	
275 280 285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg	912

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt 963  
 Pro Ala Asp Leu Leu Asp Ser  
 305 310

<210> 844

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu  
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys  
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu  
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln  
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg  
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg  
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp  
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg  
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser  
 245 250 255

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu  
 260 265 270  
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn  
 275 280 285  
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
 290 295 300  
 Pro Ala Asp Leu Leu Asp Ser  
 305 310

<210> 845  
 <211> 956  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(933)  
 <223> FRXA00306

<400> 845  
 gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48  
 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15  
 gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30  
 gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45  
 cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192  
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60  
 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240  
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80  
 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288  
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95  
 tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336  
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110  
 gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384  
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu  
 115 120 125  
 gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag 432  
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys  
 130 135 140

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gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
145                      150                      155                      160

gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
165                      170                      175

tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
180                      185                      190

acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
195                      200                      205

ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
210                      215                      220

gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
225                      230                      235                      240

acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
245                      250                      255

atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
260                      265                      270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
275                      280                      285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
290                      295                      300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
Pro Ala Asp Leu Leu Asp Ser
305                      310

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&lt;210&gt; 846

&lt;211&gt; 311

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 846

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Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1                      5                      10                      15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
20                      25                      30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
35                      40                      45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

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50	55	60
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala		
65	70	75 80
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly		
	85	90 95
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr		
	100	105 110
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu		
	115	120 125
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys		
	130	135 140
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu		
145	150	155 160
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln		
	165	170 175
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg		
	180	185 190
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg		
	195	200 205
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp		
	210	215 220
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg		
225	230	235 240
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser		
	245	250 255
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu		
	260	265 270
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn		
	275	280 285
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu		
	290	295 300
Pro Ala Asp Leu Leu Asp Ser		
305	310	

&lt;210&gt; 847

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(796)

&lt;223&gt; RXC01715

&lt;400&gt; 847

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acatgttggt ggaacatgcc ggcagagccg acactacgat tcattcgcta aagggtctgg 60

ccactgacac tggcaaagat ccacgaaagg aagttaccct gtg agc gag ctc gat 115
                                   Val Ser Glu Leu Asp
                                   1 5

att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
              10              15              20

cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp
              25              30              35

caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
              40              45              50

gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
              55              60              65

atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
              70              75              80              85

gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe
              90              95              100

tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac 451
Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His
              105              110              115

ttg cct tca ttc atc atg ggt gaa gaa gca aag gac tgg atc act gtt 499
Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys Asp Trp Ile Thr Val
              120              125              130

tac ccg ttc gtg cgc agc tac gac tgg tac atc atg gag ccc ttg aag 547
Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile Met Glu Pro Leu Lys
              135              140              145

cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595
Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro
              150              155              160              165

gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643
Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu
              170              175              180

tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691
Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu
              185              190              195

atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739
Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
              200              205              210

ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag 787
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys

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215                                      220                                      225  
 gtt ctt cct taaaagctgc ttttctaaac gat                                      819  
 Val Leu Pro  
 230  
  
 <210> 848  
 <211> 232  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 848  
 Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser  
   1                                      5                                      10                                      15  
 Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg  
                                     20                                      25                                      30  
 Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala  
                                     35                                      40                                      45  
 Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg  
                                     50                                      55                                      60  
 Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp  
   65                                      70                                      75                                      80  
 Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln  
                                     85                                      90                                      95  
 Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu  
                                     100                                      105                                      110  
 Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys  
                                     115                                      120                                      125  
 Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile  
   130                                      135                                      140  
 Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala  
   145                                      150                                      155                                      160  
 Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala  
                                     165                                      170                                      175  
 Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His  
                                     180                                      185                                      190  
 Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu  
                                     195                                      200                                      205  
 His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile  
                                     210                                      215                                      220  
 Ala Asp Leu Ile Lys Val Leu Pro  
   225                                      230  
  
 <210> 849  
 <211> 1587

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1564)

&lt;223&gt; RXN00420

&lt;400&gt; 849

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attcgtgaac tcatggatct ttaggcaata aatgtgagat tggacgattt cacgcttgtc 60

ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
                                         Met Asn Ser Ser His
                                         1           5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
                        10                15                20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
                        25                30                35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
                        40                45                50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
                        55                60                65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
                        70                75                80                85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
                        90                95                100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
                        105                110                115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
                        120                125                130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
                        135                140                145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
                        150                155                160                165

gtg gtc tcc atg gaa ctc ctc gtt gca gac gga cgc atc ctg cac ctc 643
Val Val Ser Met Glu Leu Leu Val Ala Asp Gly Arg Ile Leu His Leu
                        170                175                180

gag cca gaa ggc acc gcc gaa gac cca cag ggc gac ctg ttc tgg gca 691
Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly Asp Leu Phe Trp Ala

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185	190	195	
acc gtt ggt ggc atg ggc ctg acc ggc atc atc gtc cgt gca cgc atc			739
Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile Val Arg Ala Arg Ile			
200	205	210	
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc			787
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg			
215	220	225	
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag			835
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu			
230	235	240	245
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag			883
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu			
250	255	260	
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt			931
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu			
265	270	275	
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag			979
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys			
280	285	290	
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg			
1027			
Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp			
295	300	305	
act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc			
1075			
Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr Ala			
310	315	320	325
atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc tac			
1123			
Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr			
330	335	340	
caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag			
1171			
Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys			
345	350	355	
ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct			
1219			
Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro			
360	365	370	
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca			
1267			
Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala			
375	380	385	
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc			
1315			
Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser			
390	395	400	405

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca  
1363

Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro  
410 415 420

ggc ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc  
1411

Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe  
425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac  
1459

Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn  
440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat  
1507

Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn  
455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt  
1555

Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu  
470 475 480 485

gag ctt tct taagaaaggg cttgaactaa aca  
1587

Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala  
1 5 10 15

His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg  
20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile  
35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro  
50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr  
65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro  
85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val  
100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr  
115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly  
 130 135 140  
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly  
 145 150 155 160  
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly  
 165 170 175  
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly  
 180 185 190  
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile  
 195 200 205  
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile  
 210 215 220  
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His  
 225 230 235 240  
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp  
 245 250 255  
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly  
 260 265 270  
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala  
 275 280 285  
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp  
 290 295 300  
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly  
 305 310 315 320  
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn  
 325 330 335  
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg  
 340 345 350  
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr  
 355 360 365  
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser  
 370 375 380  
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn  
 385 390 395 400  
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp  
 405 410 415  
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys  
 420 425 430  
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg  
 435 440 445  
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp

450                      455                      460  
 Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp  
 465                      470                      475                      480  
 Met Ser Arg Arg Leu Glu Leu Ser  
 485  
  
 <210> 851  
 <211> 563  
 <212> DNA  
 <213> *Corynebacterium glutamicum*  
  
 <220>  
 <221> CDS  
 <222> (1)..(540)  
 <223> FRXA00420  
  
 <400> 851  
 tgg act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac 48  
 Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr  
 1                      5                      10                      15  
 gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc 96  
 Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe  
 20                      25                      30  
 tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc 144  
 Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser  
 35                      40                      45  
 aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag 192  
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu  
 50                      55                      60  
 cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc 240  
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser  
 65                      70                      75                      80  
 gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg 288  
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu  
 85                      90                      95  
 tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc 336  
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg  
 100                      105                      110  
 cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa 384  
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu  
 115                      120                      125  
 ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag 432  
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu  
 130                      135                      140  
 aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga 480  
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg  
 145                      150                      155                      160  
 aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga 528

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg  
 165 170 175

ctt gag ctt tct taagaaaggg cttgaactaa aca 563  
 Leu Glu Leu Ser  
 180

<210> 852

<211> 180

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 852

Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr  
 1 5 10 15

Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe  
 20 25 30

Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser  
 35 40 45

Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu  
 50 55 60

Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser  
 65 70 75 80

Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu  
 85 90 95

Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg  
 100 105 110

Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu  
 115 120 125

Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu  
 130 135 140

Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg  
 145 150 155 160

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg  
 165 170 175

Leu Glu Leu Ser  
 180

<210> 853

<211> 622

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(622)

<223> FRXA00426

&lt;400&gt; 853

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ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
                                         Met Asn Ser Ser His
                                         1           5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
                        10                        15                        20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
                        25                        30                        35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
                        40                        45                        50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
                        55                        60                        65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
                        70                        75                        80                        85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
                        90                        95                        100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
                        105                        110                        115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
                        120                        125                        130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
                        135                        140                        145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
                        150                        155                        160                        165

gtg gtc tcc atg gaa ctc ctc gtt gca 622
Val Val Ser Met Glu Leu Leu Val Ala
                        170

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&lt;210&gt; 854

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 854

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Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
  1           5           10           15

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His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg  
                   20                                  25                                  30  
 Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile  
                   35                                  40                                  45  
 Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro  
                   50                                  55                                  60  
 Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr  
                   65                                  70                                  75                                  80  
 Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro  
                                   85                                  90                                  95  
 Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val  
                                   100                                  105                                  110  
 Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr  
                   115                                  120                                  125  
 Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly  
                   130                                  135                                  140  
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly  
                   145                                  150                                  155                                  160  
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala  
                                   165                                  170

&lt;210&gt; 855

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; RXN00708

&lt;400&gt; 855

cctgcgtatc ggctgccttt ttgaattctt ttcctcctcg aggcctaacc ttcaattcct 60  
 taccgateccc cttccctgaa gtttcgctaa cctggcggtac atg act ctt tcc ctt 115  
   Met Thr Leu Ser Leu  
   1                                  5  
 cct cca att ggt ttc ggc acc gtt cat ctt gat ggc gca cct ggc gtt 163  
 Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp Gly Ala Pro Gly Val  
                                   10                                  15                                  20  
 gaa gcc atc gct act gcc att gat gct ggt tac cgc ctc atc gac acc 211  
 Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr Arg Leu Ile Asp Thr  
                                   25                                  30                                  35  
 gcg tac aac tat gaa aat gaa ggt acc gtg ggc aag gct gtc cgc gag 259  
 Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly Lys Ala Val Arg Glu  
                                   40                                  45                                  50  
 tcg ggt gtc ccc cgc gag gaa ttg att gtt acc agt aag ctc cct ggc 307

Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly		
55						60					65						
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355	
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu		
70					75					80					85		
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403	
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro		
				90					95					100			
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451	
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu		
			105					110					115				
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499	
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu		
		120					125					130					
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggg	gaa	ctg	ccg	gcc	547	
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala		
		135				140					145						
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595	
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val		
150					155				160						165		
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643	
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu		
				170					175					180			
agc	aac	ggg	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691	
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly		
			185					190					195				
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739	
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His		
		200					205					210					
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787	
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln		
		215				220					225						
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835	
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val		
230					235					240					245		
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883	
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln		
			250					255					260				
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagtta	catcaagggtt	ccg						930	
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe										
			265														

&lt;210&gt; 856

&lt;211&gt; 269

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 856

Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp  
 1 5 10 15

Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr  
 20 25 30

Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly  
 35 40 45

Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr  
 50 55 60

Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg  
 65 70 75 80

Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu  
 85 90 95

Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp  
 100 105 110

Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly  
 115 120 125

Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr  
 130 135 140

Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro  
 145 150 155 160

Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu  
 165 170 175

Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu  
 180 185 190

Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala  
 195 200 205

Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr  
 210 215 220

Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu  
 225 230 235 240

Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly  
 245 250 255

Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe  
 260 265

&lt;210&gt; 857

&lt;211&gt; 695

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(672)

&lt;223&gt; FRXA00708

&lt;400&gt; 857

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acc gtg ggc aag gct gtc cgc gag tcg ggt gtc ccc cgc gag gaa ttg   48
Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu
   1             5             10             15

att gtt acc agt aag ctc cct ggc cgc ttc cat gct cgc gat cta gga   96
Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly
             20             25             30

cgc gtc cgc att gag gaa agt cta tac cgc ctc aac tta gat tac atc   144
Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
             35             40             45

gat ctc ctc ttg att cac tgg cct aat ccc agc aag gat ctc tac gtc   192
Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
             50             55             60

gag gcg tgg gaa acg ctg att gaa gtc cgc gat gct ggc ctg gtc aag   240
Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
   65             70             75             80

cac atc gga gtg tct aac ttc ctt cca aat cac att gat cgc ctg cgc   288
His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
             85             90             95

cgc gaa acc ggt gaa ctg ccg gcc gtt aac cag atc gag ttg cac ccc   336
Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
             100            105            110

tat ttc ccg cag gtg gag cag gta gat ttc cac gat gag ctg ggc atc   384
Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
             115            120            125

att acc gag gcc tgg agc ccg ctc agc aac ggt cgc gga ctc gtc gaa   432
Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
             130            135            140

gag cca ttg ctc aag gaa atc ggc gag cgc tac ggg gtc ggc agc ggc   480
Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
             145            150            155            160

gaa atc gcc ctc gct tgg cat cac gcc agg gga atc gtt ccg att cca   528
Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
             165            170            175

cgc tcc acc aac ccg gcc agg cag cgc agc aac ttg gag gcg gta aag   576
Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
             180            185            190

att tcg ctt atc gac gaa gac gtc cag gcg att acc gct ttg gcg cgc   624
Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
             195            200            205

aaa aac ggc cgg atc aaa gat caa gat cca gcc gtc tat gaa gaa ttc   672
Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
             210            215            220

tagatagtta catcaagggtt ccg   695

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&lt;210&gt; 858

&lt;211&gt; 224

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 858

Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu  
 1 5 10 15

Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly  
 20 25 30

Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile  
 35 40 45

Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val  
 50 55 60

Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys  
 65 70 75 80

His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg  
 85 90 95

Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro  
 100 105 110

Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile  
 115 120 125

Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu  
 130 135 140

Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly  
 145 150 155 160

Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro  
 165 170 175

Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys  
 180 185 190

Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg  
 195 200 205

Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe  
 210 215 220

&lt;210&gt; 859

&lt;211&gt; 1038

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1015)

&lt;223&gt; RXA02373

&lt;400&gt; 859

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aaagtcata g ctcattgtaa ttcagtgtag ataggcgtac ggtgggctat ccaattcatc 60

tcaacctaag ggcatttttg gtgcgcacatca aggagaaaaat atg tct gtt gtg ggt 115
Met Ser Val Val Gly
1 5

acc ggc cta ttc ttt gga tcc ccg gag gaa gag cgg gat aag ttg atg 163
Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu Arg Asp Lys Leu Met
10 15 20

caa tct ttg atg gat cag aag aat aag ctt tcg aag tct gaa ggt atc 211
Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
25 30 35

cca ttg gtc acc ttg aat gat gga aaa acc att cct cag ctt ggt ttt 259
Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile Pro Gln Leu Gly Phe
40 45 50

ggt gtg ttc aag gta gat ccc gat gaa gca gag cgc gta gtt acc gaa 307
Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
55 60 65

gca ctt gag gta ggt tac cgc cac atc gat act gct gcg att tac ggc 355
Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
70 75 80 85

aat gag gaa ggt gtc ggc cga gct att gct aag tcc ggc att cct cgt 403
Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys Ser Gly Ile Pro Arg
90 95 100

gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
105 110 115

gta gaa gct gct ttt gag gag tct ctg cag aag ctg ggc ttg gat tat 499
Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
120 125 130

gta gat ctg tac ttg gtg cac tgg ccg gca ccg aag aac gat aat tat 547
Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro Lys Asn Asp Asn Tyr
135 140 145

gtt gct gca tgg aag ggc ttg gaa aag ctc ggt gac cgt gct cgt tcc 595
Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly Asp Arg Ala Arg Ser
150 155 160 165

atc ggt gtg tgc aac ttc ctg cca gag cac cta gaa aag ctg ctg gca 643
Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
170 175 180

gag gca acc act gtg cct gcc att aac cag att gag ctg cac cca gct 691
Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
185 190 195

ttg cag cag cgc gat gct gtt gag gca tct ctt gca gca ggc atc act 739
Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu Ala Ala Gly Ile Thr
200 205 210

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gtg gag tcg tgg ggt cct ctg gga cag ggg cgt ttt gat ctt ggc gct 787  
 Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg Phe Asp Leu Gly Ala  
 215 220 225

gag gaa cca atc gca gct gca gcg aag aac cat gga aag acc cca gct 835  
 Glu Glu Pro Ile Ala Ala Ala Lys Asn His Gly Lys Thr Pro Ala  
 230 235 240 245

cag gtt gtt atc cgt tgg cac ctg cag aac ggt ttc gtt gtg ttc ccc 883  
 Gln Val Val Ile Arg Trp His Leu Gln Asn Gly Phe Val Val Phe Pro  
 250 255 260

aag act gtg act aag agc cgc atg gtg gaa aac atc gac gtg ttt gat 931  
 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp  
 265 270 275

ttc gaa ctc agt gat gag gag atg gct gcg atc act gct ctt gag cgc 979  
 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg  
 280 285 290

aat gat cgt ggt ggt tca cac ccg aat gat ctg aac tagaaataag  
 1025  
 Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu Asn  
 295 300 305

gtaaggccct gca  
 1038

<210> 860

<211> 305

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 860

Met Ser Val Val Gly Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu  
 1 5 10 15

Arg Asp Lys Leu Met Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser  
 20 25 30

Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile  
 35 40 45

Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu  
 50 55 60

Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr  
 65 70 75 80

Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys  
 85 90 95

Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn  
 100 105 110

Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys  
 115 120 125

Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro  
 130 135 140

Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly  
 145 150 155 160  
 Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu  
 165 170 175  
 Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile  
 180 185 190  
 Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu  
 195 200 205  
 Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg  
 210 215 220  
 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His  
 225 230 235 240  
 Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly  
 245 250 255  
 Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn  
 260 265 270  
 Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile  
 275 280 285  
 Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu  
 290 295 300  
 Asn  
 305

<210> 861  
 <211> 1683  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1660)  
 <223> RXS00389

<400> 861  
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 tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115  
 Met Ile Thr Ala Thr  
 1 5  
 gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163  
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys  
 10 15 20  
 aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211  
 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn  
 25 30 35  
 cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259



Pro	Ser	Tyr	Ser	Leu	Ala	Asn	Ser	Ala	Gln	Leu	Arg	Ala	Ala	Thr	Thr		
		40					45					50					
tcg	gcg	aag	cga	gct	ttt	gaa	agc	tac	cga	ctc	act	act	cca	gag	gtt	307	
Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val		
	55					60				65							
aga	gca	gat	ttc	ctg	gat	tcc	atc	gct	gac	aac	atc	gat	gcg	cta	tcc	355	
Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser		
70					75					80					85		
ggc	gag	atc	gtg	caa	cgg	gcg	agc	ctg	gag	aca	ggg	ttg	gga	act	acc	403	
Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr		
				90					95					100			
cga	ctc	aca	ggc	gaa	gta	gcc	cgc	acc	agc	aac	cag	ctc	cgc	ctg	ttt	451	
Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe		
			105					110					115				
gca	gaa	acc	gtg	aga	agc	gga	cag	ttc	cac	cga	gta	cgc	att	gaa	cga	499	
Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg		
	120						125					130					
gga	ccg	cgg	att	gat	ctt	cgc	cag	cgt	cag	gtt	ccg	ttg	gga	cca	gtc	547	
Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val		
	135					140					145						
gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggg	595	
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly		
150					155				160						165		
ggc	gat	aca	gca	tca	gcg	ttg	gct	gca	ggc	tgc	cct	gtg	gtt	ttt	aag	643	
Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys		
				170					175						180		
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691	
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val		
			185					190					195				
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggg	gtg	ttt	aac	ctt	739	
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu		
	200						205					210					
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcg	gat	ccg	787	
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro		
	215					220					225						
aat	atc	acg	gca	atc	ggg	ttt	acc	ggg	tca	cgc	cag	ggg	ggg	ttg	gca	835	
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala		
230					235					240				245			
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883	
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala		
				250					255					260			
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931	
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala		
			265					270					275				
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979	
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val		

280	285	290
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc 1027		
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 305		
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075		
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325		
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag 1123		
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln 330 335 340		
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171		
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355		
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg 1219		
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro 360 365 370		
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg 1267		
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu 375 380 385		
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc 1315		
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405		
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca 1363		
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415 420		
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt 1411		
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459		
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp 440 445 450		
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507		
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr 455 460 465		
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555		
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile 470 475 480 485		

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg  
1603

Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu  
490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa  
1651

Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu  
505 510 515

ata gac cgt taatagctgg tctttacatt tgc  
1683

Ile Asp Arg  
520

<210> 862

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 862

Met Ile Thr Ala Thr Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu  
1 5 10 15

Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr  
20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu  
35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu  
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn  
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr  
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn  
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg  
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val  
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala  
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys  
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu  
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala  
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu  
 210 215 220  
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg  
 225 230 235 240  
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro  
 245 250 255  
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe  
 260 265 270  
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala  
 275 280 285  
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro  
 290 295 300  
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala  
 305 310 315 320  
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr  
 325 330 335  
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala  
 340 345 350  
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu  
 355 360 365  
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu  
 370 375 380  
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val  
 385 390 395 400  
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu  
 405 410 415  
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln  
 420 425 430  
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val  
 435 440 445  
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile  
 450 455 460  
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val  
 465 470 475 480  
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr  
 485 490 495  
 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp  
 500 505 510  
 Ala Val Pro Arg Glu Ile Asp Arg  
 515 520

<210> 863  
 <211> 882  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(859)  
 <223> RXS00419

<400> 863  
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 gccgacttga gctttcttaa gaaagggcctt gaactaaaca atg ctt aac gca gtg 115  
 Met Leu Asn Ala Val  
 1 5  
 ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt 163  
 Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly  
 10 15 20  
 att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc 211  
 Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr  
 25 30 35  
 ttg gca gcg cgt aaa gat tcc cca cgc gtg gac gca gca gtc gca gag 259  
 Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu  
 40 45 50  
 atc aaa gca gct ggc gct gct tcc gtt gct gtt gtt gat ttc gat gcg 307  
 Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val Val Asp Phe Asp Ala  
 55 60 65  
 ctc gac acc gaa tcc cac cct gca gcc atc gac gca gcc ttt gaa aac 355  
 Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp Ala Ala Phe Glu Asn  
 70 75 80 85  
 ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac 403  
 Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn  
 90 95 100  
 gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc acc gtg 451  
 Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val  
 105 110 115  
 aac tac acc gcc ggc ggt tcc gta ggt gta ctg ctg ggc cag aaa ttt 499  
 Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe  
 120 125 130  
 gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg gca ggc 547  
 Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly  
 135 140 145  
 cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag gca ggt 595  
 Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly  
 150 155 160 165  
 ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga tcc ggt 643  
 Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly  
 170 175 180

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691  
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser  
 185 190 195  
  
 gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739  
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala  
 200 205 210  
  
 gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787  
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val  
 215 220 225  
  
 cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835  
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg  
 230 235 240 245  
  
 gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882  
 Ala Ile Phe Arg Lys Leu Pro Phe  
 250

&lt;210&gt; 864

&lt;211&gt; 253

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 864

Met Leu Asn Ala Val Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly  
 1 5 10 15  
  
 Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly  
 20 25 30  
  
 Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp  
 35 40 45  
  
 Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val  
 50 55 60  
  
 Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp  
 65 70 75 80  
  
 Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly  
 85 90 95  
  
 Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val  
 100 105 110  
  
 Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu  
 115 120 125  
  
 Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu  
 130 135 140  
  
 Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly  
 145 150 155 160  
  
 Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala  
 165 170 175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val  
 180 185 190  
 Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn  
 195 200 205  
 Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys  
 210 215 220  
 Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe  
 225 230 235 240  
 Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe  
 245 250

&lt;210&gt; 865

&lt;211&gt; 1673

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1650)

&lt;223&gt; RXC00416

&lt;400&gt; 865

ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct	48
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala	
1 5 10 15	
att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac	96
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp	
20 25 30	
cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc	144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly	
35 40 45	
ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga	192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly	
50 55 60	
tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt	240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly	
65 70 75 80	
tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct	288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala	
85 90 95	
tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg	336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val	
100 105 110	
gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat	384
Ala Thr Gly Ile Ala Leu Val Thr Cys Ile Ile ttg gca Ala Met Asn	
115 120 125	
tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg	432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met	

130	135	140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc			480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala			
145	150	155	160
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc			528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe			
	165	170	175
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg			576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala			
	180	185	190
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg			624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu			
	195	200	205
ggg ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt			672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu			
	210	215	220
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac			720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His			
	225	230	235
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca			768
Tyr Leu Pro Leu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser			
	245	250	255
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg			816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val			
	260	265	270
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg			864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val			
	275	280	285
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac			912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn			
	290	295	300
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc			960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala			
	305	310	315
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat			1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr			
	325	330	335
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc			1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr			
	340	345	350
aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa			1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln			
	355	360	365



gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat  
1152  
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp  
370 375 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca  
1200  
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala  
385 390 395 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag  
1248  
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu  
405 410 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac  
1296  
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr  
420 425 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg  
1344  
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro  
435 440 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc  
1392  
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile  
450 455 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg  
1440  
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu  
465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc  
1488  
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser  
485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg  
1536  
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu  
500 505 510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg  
1584  
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro  
515 520 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg  
1632  
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val  
530 535 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa  
1673  
Val Val Thr His Asn Glu  
545 550

&lt;210&gt; 866

&lt;211&gt; 550

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 866

Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala  
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Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp  
 20 25 30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly  
 35 40 45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly  
 50 55 60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly  
 65 70 75 80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala  
 85 90 95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val  
 100 105 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn  
 115 120 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met  
 130 135 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala  
 145 150 155 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe  
 165 170 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala  
 180 185 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu  
 195 200 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu  
 210 215 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His  
 225 230 235 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser  
 245 250 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val  
 260 265 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val  
 275 280 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn

290	295	300
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320		
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val 530 535 540		
Val Val Thr His Asn Glu 545 550		

&lt;210&gt; 867

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1036)

&lt;223&gt; RXC02206

&lt;400&gt; 867

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ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60

accttatgac ctcagtagtg tggtagggcgt gaaacagcga atg gtc ggt tca agt 115
                                         Met Val Gly Ser Ser
                                         1           5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                        10                15                20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
                        25                30                35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
                        40                45                50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
                        55                60                65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
                        70                75                80                85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
                        90                95                100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
                        105                110                115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
                        120                125                130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
                        135                140                145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
                        150                155                160                165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
                        170                175                180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
                        185                190                195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
                        200                205                210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr

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215                      220                      225  
 gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835  
 Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile  
 230                      235                      240                      245  
 att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883  
 Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro  
 250                      255                      260  
 gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931  
 Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala  
 265                      270                      275  
 gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag 979  
 Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys  
 280                      285                      290  
 gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat  
 1027  
 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp  
 295                      300                      305  
 gtc tcc ctg tgacttggtc caattacatt cac  
 1059  
 Val Ser Leu  
 310  
  
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 <211> 312  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 868  
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 Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe  
 20                      25                      30  
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn  
 35                      40                      45  
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala  
 50                      55                      60  
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn  
 65                      70                      75                      80  
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu  
 85                      90                      95  
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu  
 100                      105                      110  
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu  
 115                      120                      125  
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr  
 130                      135                      140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala  
 145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln  
 165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro  
 180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly  
 195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser  
 210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp  
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly  
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg  
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu  
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr  
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Gln Ala Leu Asp Asp Val Ser Leu  
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<210> 869  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(598)  
 <223> RXS03074

<400> 869  
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 Met Thr Gln Ser Ala  
 1 5  
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35  
 ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
                     40                                    45                                    50  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
                     55                                    60                                    65  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
                     70                                    75                                    80                                    85  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                                     90                                    95                                    100  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                                     105                                    110                                    115  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
                                     120                                    125                                    130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
                     135                                    140                                    145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
                                     150                                    155                                    160                                    165  
 cag taatttgttt tgacgacgca gta 621  
 Gln

&lt;210&gt; 870

&lt;211&gt; 166

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 870

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
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 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
                     20                                    25                                    30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
                     35                                    40                                    45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
                     50                                    55                                    60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
                     65                                    70                                    75                                    80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                     85                                    90                                    95  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr

100	105	110	
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr			
115	120	125	
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe			
130	135	140	
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr			
145	150	155	160
Glu Ala Pro Ile Lys Gln			
165			
<210> 871			
<211> 621			
<212> DNA			
<213> <i>Corynebacterium glutamicum</i>			
<220>			
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<222> (101)..(598)			
<223> FRXA02906			
<400> 871			
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		Met Thr Gln Ser Ala	
		1 5	
cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163			
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn			
10 15 20			
gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211			
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu			
25 30 35			
ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259			
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu			
40 45 50			
ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307			
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile			
55 60 65			
gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355			
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala			
70 75 80 85			
gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403			
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala			
90 95 100			
att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451			
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala			
105 110 115			
ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499			



Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
 cag taatttggtt tgacgacgca gta 621  
 Gln

<210> 872  
 <211> 166  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 872  
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 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
           85                          90                          95  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
           100                          105                          110  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
           115                          120                          125  
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
           130                          135                          140  
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
           145                          150                          155                          160  
 Glu Ala Pro Ile Lys Gln  
                           165

<210> 873  
 <211> 1752  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1729)

&lt;223&gt; RXA02315

&lt;400&gt; 873

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gaatcgatc cgtacctgga gacgatctag actgttgtgc atg tcc agc acg cca 115
Met Ser Ser Thr Pro
1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tgc ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
55 60 65

ccg gtg gct gtg gtg atg acc tcc gcc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
135 140 145

gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
150 155 160 165

gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
170 175 180

tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
185 190 195

gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739

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Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
	215					220					225						
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly		Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270						275			
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc		
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
	295					300					305						
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt		
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg	gcc	gat	ggc	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggc	ttc		
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc		
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg		
1219																	
Asp	Thr	Leu	Phe	Ala	Ala	Ala	Ser	Asn	Ser	Ile	Arg	Asp	Leu	Ser	Leu		
		360					365					370					
gtg	ggc	atg	cct	ttt	gat	ggc	gtg	gat	acc	ttc	tcc	cca	cga	ggc	gtc		
1267																	
Val	Gly	Met	Pro	Phe	Asp	Gly	Val	Asp	Thr	Phe	Ser	Pro	Arg	Gly	Val		
	375					380					385						
gca	ggc	att	gat	ggc	tct	gtt	gct	caa	gca	atc	ggc	act	tca	ctt	gct		
1315																	
Ala	Gly	Ile	Asp	Gly	Ser	Val	Ala	Gln	Ala	Ile	Gly	Thr	Ser	Leu	Ala		
390					395					400					405		
gtg	cag	tcc	cgc	cac	ccc	gat	gaa	atc	cgc	gcg	cca	cgc	act	gtg	gcc		
1363																	
Val	Gln	Ser	Arg	His	Pro	Asp	Glu	Ile	Arg	Ala	Pro	Arg	Thr	Val	Ala		

410 415 420  
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc  
 1411  
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile  
 425 430 435  
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac  
 1459  
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn  
 440 445 450  
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt  
 1507  
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly  
 455 460 465  
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc  
 1555  
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser  
 470 475 480 485  
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac  
 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
 490 495 500  
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
 1651  
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
 505 510 515  
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca  
 1699  
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala  
 520 525 530  
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt  
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 <212> PRT  
 <213> Corynebacterium glutamicum  
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 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala  
 50 55 60  
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala  
 65 70 75 80  
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile  
 85 90 95  
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr  
 100 105 110  
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala  
 115 120 125  
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu  
 130 135 140  
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala  
 145 150 155 160  
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu  
 165 170 175  
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val  
 180 185 190  
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala  
 195 200 205  
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr  
 210 215 220  
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu  
 225 230 235 240  
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro  
 245 250 255  
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu  
 260 265 270  
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr  
 275 280 285  
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
 290 295 300  
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
 305 310 315 320  
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn  
 325 330 335  
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
 340 345 350  
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile  
 355 360 365  
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe

370					375					380					
Ser 385	Pro	Arg	Gly	Val	Ala 390	Gly	Ile	Asp	Gly	Ser 395	Val	Ala	Gln	Ala	Ile 400
Gly	Thr	Ser	Leu	Ala 405	Val	Gln	Ser	Arg	His 410	Pro	Asp	Glu	Ile	Arg 415	Ala
Pro	Arg	Thr	Val 420	Ala	Leu	Leu	Gly	Asp 425	Leu	Ser	Phe	Leu	His 430	Asp	Ile
Gly	Gly	Leu 435	Leu	Ile	Gly	Pro	Asp 440	Glu	Pro	Arg	Pro	Glu 445	Asn	Leu	Thr
Ile 450	Val	Val	Ser	Asn	Asp 455	Asn	Gly	Gly	Gly	Ile	Phe 460	Glu	Leu	Leu	Glu
Thr 465	Gly	Ala	Asp	Gly 470	Leu	Arg	Pro	Asn	Phe	Glu 475	Arg	Ala	Phe	Gly	Thr 480
Pro	His	Asp	Ala	Ser 485	Ile	Ala	Asp	Leu	Cys 490	Ala	Gly	Tyr	Gly	Ile 495	Glu
His	Gln	Val 500	Val	Asp	Asn	Leu	Gln	Asp 505	Leu	Ile	Ile	Ala	Leu 510	Val	Asp
Thr	Thr	Glu 515	Val	Ser	Gly	Phe	Thr 520	Ile	Ile	Glu	Ala	Ser 525	Thr	Val	Arg
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1057)
<223> RXA02319
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Met Ser Asn Tyr Ser
1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
40 45 50

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gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac	307
Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His	
55 60 65	
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc	355
Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly	
70 75 80 85	
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa	403
Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln	
90 95 100	
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc	451
Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg	
105 110 115	
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa	499
Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys	
120 125 130	
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc	547
Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg	
135 140 145	
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc	595
Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly	
150 155 160 165	
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc	643
Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg	
170 175 180	
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac	691
Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp	
185 190 195	
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac	739
Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn	
200 205 210	
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg	787
Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met	
215 220 225	
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa	835
Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu	
230 235 240 245	
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc	883
Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr	
250 255 260	
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc	931
Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu	
265 270 275	
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg	979
Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met	
280 285 290	

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atggggtcct  
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
310 315

aaa  
1080

<210> 876

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 876

Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala  
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Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His  
20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg  
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr  
210 215 220



Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp  
 225 230 235 240  
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn  
 245 250 255  
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu  
 260 265 270  
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr  
 275 280 285  
 Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe  
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 305 310 315

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(994)  
 <223> RXS00393

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 Met Ser His Thr Glu  
 1 5  
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
 10 15 20  
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
 25 30 35  
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259  
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
 40 45 50  
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
 55 60 65  
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355  
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
 70 75 80 85  
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451  
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595  
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met  
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
 170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
 200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
 250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile  
 265 270 275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg gcc ctg 979  
 Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu  
 280 285 290

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc  
 1017  
 Ala Leu Ala Phe Ser  
 295

&lt;210&gt; 878

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 878

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

1	5	10	15
Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

&lt;210&gt; 879

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(982)

&lt;223&gt; FRXA00393

&lt;400&gt; 879

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aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115
                                         Met Ser His Thr Glu
                                         1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
                        10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
                        25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
                        40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
                        55 60 65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
                        70 75 80 85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
                        90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
                        105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
                        120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggc 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
                        135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
                        150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
                        170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
                        185 190 195

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aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
      200                      205                      210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
      215                      220                      225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
      230                      235                      240                      245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
      250                      255                      260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
      265                      270                      275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
      280                      285                      290

cat tagcgttttag ctaaaacgct ttt
1005
His

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<210> 880
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

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      20                      25                      30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
      35                      40                      45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
      50                      55                      60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
      65                      70                      75                      80

Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
      85                      90                      95

Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
      100                      105                      110

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
      115                      120                      125

Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

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130	135	140
Tyr Gly Tyr Arg Gly	Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	
145	150	155 160
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser		
	165	170 175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly		
	180	185 190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr		
	195	200 205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys		
	210	215 220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu		
	225	230 235 240
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu		
	245	250 255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp		
	260	265 270
Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro		
	275	280 285
Cys Ser Arg Ala Trp His		
	290	

<210> 881  
 <211> 843  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(820)  
 <223> RXA00391

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tttctctccc atccctgtac aagataaaaac ccgtgcacag ttg ctg cgc gat tct	115
Leu Leu Arg Asp Ser	
1 5	
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc	163
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala	
10 15 20	
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg	211
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu	
25 30 35	
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa	259
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu	
40 45 50	

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ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
55 60 65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu
90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
230 235 240

tgc 843

<210> 882
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 882
Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
1 5 10 15

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Ala	Leu	Val	Met	Ala	Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	
			20				25						30			
Gln	Leu	Thr	Pro	Leu	Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	
			35				40						45			
Phe	Leu	Gly	Gly	Glu	Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	
			50				55						60			
Ile	Ala	Gly	Met	Gln	Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	
			65				70						75			
Pro	Leu	Ala	Ile	Asp	Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	
				85				90						95		
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser	
			100				105						110			
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile	
			115				120						125			
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu	
			130				135						140			
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val	
			145				150						155			
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly	
				165				170						175		
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu	
			180				185						190			
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His	
			195				200						205			
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu	
			210				215						220			
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His	
			225				230						235			
													240			

<210> 883

<211> 384

<212> DNA

<213> *Corynebacterium glutamicum*

**<220>**

<221> CDS

$\langle 222 \rangle$  (101) .. (361)

<223> RXS02908

<400> 883

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gtgactggtc gcgtggatac ccgtcattga ttccggtgga ttg aag ttg cac cca 115  
Leu Lys Leu His Pro



```

                                1      5
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala
      10      15      20

tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala
      25      30      35

gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp
      40      45      50

gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser
      55      60      65

ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys
      70      75      80      85

ctg ttt tagtcttcat tcttgctggc tgc 384
Leu Phe

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<210> 884  
 <211> 87  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 884
Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
 1      5      10      15

Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
      20      25      30

Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
      35      40      45

Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
      50      55      60

Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
      65      70      75      80

Arg Ala Ile Ala Lys Leu Phe
      85

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<210> 885  
 <211> 705  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(682)  
 <223> RXA00997

&lt;400&gt; 885

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gcaccatgggt gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
                                     Met Thr Thr Trp Lys
                                     1      5

gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                10                15                20

tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                25                30                35

ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                40                45                50

tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                55                60                65

gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                70                75                80                85

gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                90                95                100

atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                105                110                115

ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                120                125                130

cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                135                140                145

cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
                150                155                160                165

ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
                170                175                180

caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
                185                190

atcttgacc tga 705

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&lt;210&gt; 886

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 886

```

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
 1           5           10           15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
          20           25           30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
          35           40           45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
          50           55           60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
          65           70           75           80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
          85           90           95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
          100          105          110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
          115          120          125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
          130          135          140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
          145          150          155          160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
          165          170          175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
          180          185          190

Lys Lys

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&lt;210&gt; 887

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(838)

&lt;223&gt; RXA02189

&lt;400&gt; 887

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aatggcaaaa atgggcacat acgatactga tgggaccaat gggaaaacct caagccacca 60

attgagccag ttctctcaag caaacggata ctggtgggat  gtg gac gcg gcc gac   115
                               Val Asp Ala Ala Asp
                               1           5

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tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tcg gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggg cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
90 95 100	
ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
105 110 115	
atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc	499
Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggg gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taaaaaacca acggcgctca ttt	861

Pro

&lt;210&gt; 888

&lt;211&gt; 246

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 888

Val	Asp	Ala	Ala	Asp	Tyr	His	Glu	Arg	His	Pro	Ser	Tyr	Leu	Gly	Thr
1				5					10					15	
Asp	Ser	Ala	His	Gly	Glu	Phe	Tyr	Trp	Cys	Pro	Glu	Met	Leu	His	Glu
			20					25					30		
Lys	Asp	Val	Arg	Leu	Leu	Gly	Thr	Pro	Ala	Ala	Leu	Ser	Gly	Lys	Lys
	35						40					45			
Ile	Leu	Glu	Ile	Gly	Cys	Gly	Ser	Ala	Pro	Cys	Ala	Arg	Trp	Leu	Ala
	50					55					60				
Asn	Asp	Val	Pro	Asn	Ala	Phe	Val	Thr	Ala	Phe	Asp	Ile	Ser	Ser	Gln
65					70					75					80
Met	Leu	Lys	Tyr	Ala	Gly	His	Asp	His	Asn	Val	His	Leu	Val	Gln	Ala
				85					90					95	
Asp	Ala	Met	Ser	Leu	Pro	Tyr	Ala	Asp	Ser	Ser	Phe	Asp	Val	Val	Phe
			100					105					110		
Ser	Val	Phe	Gly	Ala	Ile	Pro	Phe	Val	Glu	Asp	Ser	Ala	Ala	Leu	Met
	115						120					125			
Lys	Glu	Ile	Ala	Arg	Val	Leu	Lys	Pro	Gly	Gly	Arg	Leu	Ile	Phe	Ser
	130					135					140				
Ile	Thr	His	Pro	Met	Arg	Trp	Ile	Phe	Leu	Asp	Asp	Pro	Gly	Pro	Ala
145					150					155					160
Gly	Leu	Thr	Ala	Ile	Thr	Ser	Tyr	Phe	Asp	Gln	Arg	Gly	Tyr	Val	Glu
				165					170					175	
Glu	Asp	Glu	Glu	Thr	Gly	Ala	Leu	Ser	Tyr	Ala	Glu	Gln	His	Arg	Thr
			180					185					190		
Met	Gly	Ala	Arg	Ile	Asn	Glu	Leu	Ile	Asp	Ala	Ser	Leu	His	Leu	Asp
	195						200					205			
His	Leu	Ile	Glu	Pro	Glu	Trp	Pro	Asp	Glu	Leu	Glu	Glu	Asn	Trp	Gly
	210					215					220				
Gln	Trp	Ser	Pro	Leu	Arg	Gly	Lys	Leu	Phe	Pro	Gly	Thr	Ala	Ile	Phe
225					230					235					240
Leu	Ala	Thr	Tyr	Arg	Pro										
				245											

&lt;210&gt; 889

&lt;211&gt; 813

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(790)

&lt;223&gt; RXA02311

&lt;400&gt; 889

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cattttgggt atcggttggt tgtccatcgg tggagctaag ggcgctaagc atcgcagcca 60

aataacctcc cactaaagct cctgggttag actcgaacgc gtg gct aaa gca gat 115
                               Val Ala Lys Ala Asp
                               1 5

tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
                               10 15 20

aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
                               25 30 35

gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
                               40 45 50

aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
                               55 60 65

gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355
Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
70 75 80 85

ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly
90 95 100

atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct 451
Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser
105 110 115

tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg 499
Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met
120 125 130

gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser
135 140 145

acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met
150 155 160 165

cgc ctg ctg ccc cag gcg gcg cgc gca gta tcg tcc aac ccg gag gcc 643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala
170 175 180

tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa 691
Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

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185	190	195	
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag			739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln			
200	205	210	
aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag			787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu			
215	220	225	
aac tagtcgagtc ccacagaggg gag			813
Asn			
230			
<210> 890			
<211> 230			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 890			
Val Ala Lys Ala Asp Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met			
1	5	10	15
Phe Asp Asp Val Gly Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser			
20	25	30	
Phe Gly Gln Asp Arg Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp			
35	40	45	
Leu Lys Pro Gly Glu Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val			
50	55	60	
Ser Thr Val Glu Leu Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp			
65	70	75	80
Phe Ser Gln Gly Met Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys			
85	90	95	
Val Val Gly Asp Gly Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp			
100	105	110	
Ala Val Thr Ile Ser Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala			
115	120	125	
Gly Leu Lys Glu Met Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr			
130	135	140	
Val Ala Glu Phe Ser Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr			
145	150	155	160
Lys Glu Tyr Leu Met Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser			
165	170	175	
Ser Asn Pro Glu Ala Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp			
180	185	190	
Pro Ser Gln Ala Glu Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser			
195	200	205	
Asp Cys Gly Trp Gln Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser			

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210                215                220

Ala Ile Lys Pro Glu Asn
225                230

<210> 891
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXN02912

<400> 891
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gatattgaaa tgacgtattc ctgattgggc tgaaaaatct gtg aca tca cct gaa 115
                Val Thr Ser Pro Glu
                1                5

tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr
                10                15                20

cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile
                25                30                35

tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg 259
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala
                40                45                50

gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu
                55                60                65

cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu
                70                75                80                85

atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt 403
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly
                90                95                100

cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc 451
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe
                105                110                115

cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr
                120                125                130

ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys
                135                140                145

cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly

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150	155	160	165	
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe				
	170	175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr				
	185	190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu				
	200	205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln				
	215	220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe				
	230	235	240	245
agg gga att aaa tcc agt tagtgctgtt ttaagcggtc gag				876
Arg Gly Ile Lys Ser Ser				
	250			

&lt;210&gt; 892

&lt;211&gt; 251

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly				
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Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln				
	20	25	30	
Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile				
	35	40	45	
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly				
	50	55	60	
Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val				
	65	70	75	80
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu				
	85	90	95	
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala				
	100	105	110	
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg				
	115	120	125	
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp				
	130	135	140	
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala				

145											150											155											160
Trp	Tyr	Pro	Lys	Gly	Ile	Asp	Ala	Gly	Thr	Glu	Val	Asp	Ser	Val	Asp																		
				165							170											175											
Gly	Pro	Ser	Ala	Phe	Val	Glu	Thr	Tyr	Thr	Pro	Glu	Leu	Leu	Arg	Asn																		
				180							185											190											
Leu	Pro	Met	Ser	Thr	Thr	Ser	Thr	Gly	His	Asn	Phe	Ala	Glu	Leu	Phe																		
				195							200											205											
His	Asn	Ala	Gly	Leu	Lys	Glu	Val	Thr	Leu	Thr	Pro	Ile	Glu	Gly	Leu																		
				210							215											220											
Ala	Glu	Leu	Asp	Gln	Arg	Phe	Gly	Leu	Ser	Pro	Gly	His	Glu	Ser	Thr																		
225											230							235											240				
Pro	Gln	Phe	Leu	Phe	Arg	Gly	Ile	Lys	Ser	Ser																							
				245							250																						

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<210> 893
<211> 585
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(562)  
<223> RXS00998
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<400> 893																		
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tgaaaatcca accatttttag gccgactaga gtaattaatt atg act tcc cgc gat																		115
Met Thr Ser Arg Asp																		
1 5																		
gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga																		163
Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg																		
10 15 20																		
gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc																		211
Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly																		
25 30 35																		
ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg																		259
Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg																		
40 45 50																		
gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc																		307
Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly																		
55 60 65																		
ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca																		355
Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser																		
70 75 80 85																		
gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac																		403
Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn																		
90 95 100																		

aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451  
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala  
                   105                                  110                                  115

gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499  
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile  
                   120                                  125                                  130

gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547  
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr  
                   135                                  140                                  145

atg gtg ctg aac aag tagccctata ctcgggcacc atg 585  
 Met Val Leu Asn Lys  
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<210> 894

<211> 154

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 894

Met Thr Ser Arg Asp Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu  
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Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn  
                   20                                  25                                  30

Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr  
           35                                  40                                  45

Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His  
           50                                  55                                  60

Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala  
           65                                  70                                  75                                  80

Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met  
                   85                                  90                                  95

Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser  
           100                                  105                                  110

Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr  
           115                                  120                                  125

His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg  
           130                                  135                                  140

Thr Thr Leu Arg Thr Met Val Leu Asn Lys  
 145                                  150

<210> 895

<211> 1098

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)..(1075)

&lt;223&gt; RXA01215

&lt;400&gt; 895

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cccaaaacgt ccacaaccag gaaggctaag caggatcctc atg act gct cac tgg 115
                                         Met Thr Ala His Trp
                                         1      5

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163
Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro
                      10                      15                      20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211
Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro
                      25                      30                      35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259
Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu
                      40                      45                      50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307
Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln
                      55                      60                      65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355
Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu
                      70                      75                      80                      85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403
Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro
                      90                      95                      100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct 451
Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala
                      105                      110                      115

cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg 499
Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val
                      120                      125                      130

tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca 547
Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro
                      135                      140                      145

gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595
Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu
                      150                      155                      160                      165

aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc 643
Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg
                      170                      175                      180

gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg 691
Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met
                      185                      190                      195

gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc 739
Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val

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200	205	210	
gcc aac cgc gtc gtc ggt gac gtc gac ggc aag gac tgc gtg ctt ctc			787
Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys Asp Cys Val Leu Leu			
215	220	225	
gac gac atg atc gac act ggc ggc acc atc gcc ggc gct gtg ggc gtc			835
Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
	250	255	260
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
	265	270	275
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
	280	285	290
aac ctg acc gtt ttg tgc atc gca ccg ctg ctg gct cgc acc atc aac			
1027			
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
	295	300	305
gag atc ttc gaa aac ggt tcc gtc acc acc ctc ttc gag ggc gag gcc			
1075			
Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu Phe Glu Gly Glu Ala			
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1098			
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<211> 325			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 896			
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Gly Arg Ala His Pro Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp			
	20	25	30
Val Asn Val Thr Pro Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile			
	35	40	45
Tyr Val Arg Phe Glu Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu			
	50	55	60
Gln Ser His Thr Gln Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu			
	65	70	75
Met Ile Asp Ala Leu Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile			
	85	90	95
Leu Pro Phe Tyr Pro Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg			

100					105					110					
Glu	Pro	Ile	Ser	Ala	Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly
	115						120					125			
Ala	Asp	Arg	Ile	Val	Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly
	130					135					140				
Phe	Phe	Asp	Gly	Pro	Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr
145					150					155					160
Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser
			165						170					175	
Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu
		180						185						190	
Gly	Asp	Ala	Pro	Met	Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val
	195						200					205			
Ala	Asn	Gln	Val	Val	Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys
	210					215					220				
Asp	Cys	Val	Leu	Leu	Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala
225					230					235					240
Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile
			245						250					255	
Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser
		260						265					270		
Ala	Cys	Gly	Ala	Glu	Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser
	275						280					285			
Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu
	290					295					300				
Ala	Arg	Thr	Ile	Asn	Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu
305				310						315					320
Phe	Glu	Gly	Glu	Ala											
				325											

&lt;210&gt; 897

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1447)

&lt;223&gt; RXN00558

&lt;400&gt; 897

gaacaggcac cgcaggaaga atgcggcggtt ttcggcggtt gggcgccagg tgaggaagtc 60

tcgaaactta cctactttgg cctcttcgca cttcagcacc gtg gtc aag aag ccc 115

Val Val Lys Lys Pro

1

5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat	163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc	211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
55 60 65	
acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
120 125 130	
aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
cgc ggc tgg gta gtc gca tct gaa acc gca gcg ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
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gcc tcg cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	

gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca 883  
 Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser  
 250 255 260

ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc 931  
 Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe  
 265 270 275

ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag 979  
 Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln  
 280 285 290

cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca  
 1027  
 Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro  
 295 300 305

ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc  
 1075  
 Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser  
 310 315 320 325

atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa  
 1123  
 Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu  
 330 335 340

gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa  
 1171  
 Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys  
 345 350 355

tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att  
 1219  
 Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile  
 360 365 370

gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc  
 1267  
 Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val  
 375 380 385

cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc  
 1315  
 Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser  
 390 395 400 405

atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc  
 1363  
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 410 415 420

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 1411  
 Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala  
 425 430 435

gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggt  
 1457  
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1470

<210> 898

<211> 449

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 898

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Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr  
35 40 45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg  
50 55 60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu  
65 70 75 80

Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val  
85 90 95

Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu  
100 105 110

Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu  
115 120 125

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly  
130 135 140

His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser  
145 150 155 160

Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala  
165 170 175

Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu  
180 185 190

Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu  
195 200 205

Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro  
210 215 220

Asp Ser Val Ile Lys Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile  
225 230 235 240

Gly Arg Lys Leu Ala Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile  
245 250 255

Pro Thr Pro Glu Ser Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala  
260 265 270

Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly  
 275 280 285  
 Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg  
 290 295 300  
 Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val  
 305 310 315 320  
 Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile  
 325 330 335  
 Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala  
 340 345 350  
 Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr  
 355 360 365  
 Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu  
 370 375 380  
 Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr  
 385 390 395 400  
 Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu  
 405 410 415  
 Leu Cys Ile Ala Cys Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln  
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 Gly Asn Ser Asn Ala Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser  
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Ser

<210> 899  
 <211> 524  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (61)..(501)  
 <223> FRXA00558

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 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile  
 1 5 10 15  
 ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156  
 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro  
 20 25 30  
 att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204  
 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

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          35              40              45
acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc 252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
      50              55              60

atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg 300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
      65              70              75              80

att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc 348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
      85              90              95

gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc 396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
      100             105             110

gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa 444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
      115             120             125

ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga 492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
      130             135             140

cac acc ctg taagcagcgc gtgatccatt cgg 524
His Thr Leu
145

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&lt;210&gt; 900

&lt;211&gt; 147

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 900

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Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
  1              5              10              15

Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
      20              25              30

Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
      35              40              45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
      50              55              60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
      65              70              75              80

Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
      85              90              95

Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
      100             105             110

Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
      115             120             125

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Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly  
 130 135 140

His Thr Leu  
 145

<210> 901

<211> 1386

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1363)

<223> RXN00626

<400> 901

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aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115  
 Met Arg Ile Leu Val  
 1 5

atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163  
 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr  
 10 15 20

gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211  
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu  
 25 30 35

gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259  
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu  
 40 45 50

gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307  
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile  
 55 60 65

ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355  
 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala  
 70 75 80 85

gcg ggt atc gct gtg ttt ggt cct aac aag gac gct gct cgt atc gag 403  
 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu  
 90 95 100

ggc tcc aag gct ttc gct aag gat gtc atg gct gcg cag ggt gtt cgt 451  
 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg  
 105 110 115

act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att 499  
 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile  
 120 125 130

gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat 547  
 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp  
 135 140 145

ggg ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595

Gly 150	Leu	Ser	Ala	Gly 155	Lys	Gly	Val	Val	Val	Thr 160	Pro	Asp	Arg	Ala	Ala 165	
gca cgt gct cac gta gat gca gtg ctt gag ggc gga aat cca gtt ttg	643															
Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly Asn Pro Val Leu																
170	175	180														
ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg ttc tgc ctg gtt	691															
Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu Phe Cys Leu Val																
185	190	195														
gat ggc gag acg gta gtt cct ctg ctg cca gcg cag gat cac aag cgt	739															
Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln Asp His Lys Arg																
200	205	210														
gcg tac gac aac gat gag ggc cca aac act ggt ggc atg ggt gct tat	787															
Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly Met Gly Ala Tyr																
215	220	225														
gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag cgc att gtc gat	835															
Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln Arg Ile Val Asp																
230	235	240	245													
gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca cgt ggt tgc gcg	883															
Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala Arg Gly Cys Ala																
250	255	260														
tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt gca gaa ggc cct	931															
Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly Ala Glu Gly Pro																
265	270	275														
gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca gaa acc cag gct	979															
Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro Glu Thr Gln Ala																
280	285	290														
gta ctg gca cta ctg aag act cct cta gca gta ctg ctc aac gca gtt																
1027																
Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu Leu Asn Ala Val																
295	300	305														
gct act gga acc ttg gca gag cag cca gca ctg gag tgg gag gat gct																
1075																
Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu Trp Glu Asp Ala																
310	315	320	325													
tac gcc ctg act gtg gtg ttg gct tct tac aac tac cca gag gca cct																
1123																
Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr Pro Glu Ala Pro																
330	335	340														
cgt act ggt gat gtc atc cgc aac gct gat gca gat aac gtt ctt cac																
1171																
Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp Asn Val Leu His																
345	350	355														
gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc tct gcg ggc ggt																
1219																
Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val Ser Ala Gly Gly																
360	365	370														

cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc  
1267

Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg  
375 380 385

gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac  
1315

Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His  
390 395 400 405

tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc  
1363

Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly Arg Ile Ser Ile  
410 415 420

taaaagcagt acgcagatag gct  
1386

<210> 902

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 902

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu  
1 5 10 15

Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro  
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys  
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser  
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala  
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp  
85 90 95

Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala  
100 105 110

Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala  
115 120 125

Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp  
130 135 140

Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr  
145 150 155 160

Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly  
165 170 175

Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser  
180 185 190

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<400> 903
tcattttaag ggcgttttcg acgccacttt caaccatttc cgaaccgccca agaatactgg 60
aatagcttgg atcaagtttt gcaggataaaa ctgtgcaacc atg cgc att ctg gta    115
                               Met Arg Ile Leu Val
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                                1           5
atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr
                        10           15           20

gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu
                        25           30           35

gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu
                        40           45           50

gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile
                        55           60           65

ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala
                        70           75           80           85

gcg ggt atc 364
Ala Gly Ile

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<210> 904  
 <211> 88  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 904
Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu
  1           5           10           15

Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
      20           25           30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
      35           40           45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
      50           55           60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
      65           70           75           80

Asp Ala Leu Arg Ala Ala Gly Ile
      85

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<210> 905  
 <211> 803  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(780)  
 <223> FRXA00626



<400> 905  
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 Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly  
 1 5 10 15

aat cca gtt ttg ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg 96  
 Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu  
 20 25 30

ttc ttc ctg gtt gat ggc gag acg gta gtt cct ctg ctg cca gcg cag 144  
 Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln  
 35 40 45

gat cac aag cgt gcg tac gac aac gat gag ggc cca aac act ggt ggc 192  
 Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly  
 50 55 60

atg ggt gct tat gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag 240  
 Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln  
 65 70 75 80

cgc att gtc gat gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca 288  
 Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala  
 85 90 95

cgt ggt tgc gcg tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt 336  
 Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly  
 100 105 110

gca gaa ggc cct gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca 384  
 Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro  
 115 120 125

gaa acc cag gct gta ctg gca cta ctg aag act cct cta gca gta ctg 432  
 Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu  
 130 135 140

ctc aac gca gtt gct act gga acc ttg gca gag cag cca gca ctg gag 480  
 Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu  
 145 150 155 160

tgg gag gat gct tac gcc ctg act gtg gtg ttg gct tct tac aac tac 528  
 Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr  
 165 170 175

cca gag gca cct cgt act ggt gat gtc atc cgc aac gct gat gca gat 576  
 Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp  
 180 185 190

aac gtt ctt cac gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc 624  
 Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val  
 195 200 205

tct gcg ggc ggt cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg 672  
 Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu  
 210 215 220

gag gct gca cgc gat aac gcg tac acc acc atc aag gac att gaa ctt 720  
 Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu  
 225 230 235 240

gag gga agc cac tac cgc agc gat atc gca ttg gct gca tta gag ggt 768  
Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
245 250 255

cgt atc tcg atc taaaagcagt acgcagatag gct 803  
 Arg Ile Ser Ile  
 260

<210> 906

**<211> 260**

<212> PRT

<213> Corynebacterium glutamicum

<400> 906

Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly  
1 5 10 15

Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu  
20 25 30

Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln  
35 40 45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly  
50 55 60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln  
65 70 75 80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala  
85 90 95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly  
100 105 110

Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro  
115 120 125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu  
130 135 140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu  
145 150 155 160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr  
165 170 175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp  
180 185 190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val  
195 200 205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu  
210 215 220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu  
225 230 235 240

Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
 245 250 255

Arg Ile Ser Ile  
 260

<210> 907

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXA02623

<400> 907

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aatgatgggt ccgaggccga agaccgttaa catatctgtt gtg aat tct gac tct 115  
 Val Asn Ser Asp Ser  
 1 5

acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163  
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln  
 10 15 20

tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211  
 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser  
 25 30 35

gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259  
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp  
 40 45 50

act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307  
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu  
 55 60 65

ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355  
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala  
 70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403  
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser  
 90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451  
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala  
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499  
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser  
 120 125 130

aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547  
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala  
 135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His  
 150 155 160 165  
 gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643  
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn  
 170 175 180  
 agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691  
 Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln Leu Asn Trp Arg Gly  
 185 190 195  
 taaatccttc atgagcgatg atc 714  
  
 <210> 908  
 <211> 197  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 908  
 Val Asn Ser Asp Ser Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr  
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 Gly Thr Leu Leu Gln Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile  
 20 25 30  
 Val Gly Val Val Ser Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala  
 35 40 45  
 Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala  
 50 55 60  
 Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp  
 65 70 75 80  
 Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu  
 85 90 95  
 Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro  
 100 105 110  
 Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val  
 115 120 125  
 Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr  
 130 135 140  
 Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp  
 145 150 155 160  
 Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile  
 165 170 175  
 Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln  
 180 185 190  
 Leu Asn Trp Arg Gly  
 195  
  
 <210> 909

&lt;211&gt; 1347

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1324)

&lt;223&gt; RXA01442

&lt;400&gt; 909

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caccaatatt tctgacatct tccaacggag gctaaaaggc atg tac atc cca gag 115
                                         Met Tyr Ile Pro Glu
                                         1           5

tcg atc ggc acc cct ttg acc ccc aat gcc acg aaa gtg atg ctg ctg 163
Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu
                        10                        15                        20

gga tca gga gaa tta ggc aaa gaa gta gcc atc gct ttc cag cgt ctc 211
Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu
                        25                        30                        35

ggc ctg gaa gtc cat gca gtt gat cgc tac gaa cat gcc cca gcc cac 259
Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His
                        40                        45                        50

cag gtc gct cac ttc tcc tat gtc atc gac atg aca gat gca gcc cag 307
Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln
                        55                        60                        65

gtg cgg gaa ttg gtg gag cgt gtg cgc cca gat ttt gtc att cct gaa 355
Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu
                        70                        75                        80                        85

atc gaa gca ctg gca acc gat gaa ctg gtg aag atc gaa gaa gag ggg 403
Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly
                        90                        95                        100

cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac 451
Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn
                        105                        110                        115

cgc gaa ggc atc cgc aag ctg gcg gca gag gaa ctg ggt ctt cca acc 499
Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu Leu Gly Leu Pro Thr
                        120                        125                        130

tcc aac tat gag ttc tgc tcc act ttc gag gaa ttc tcc gca gct gct 547
Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala
                        135                        140                        145

gaa aag ctt ggt tac ccc aac gtg gtg aaa cca gtg atg agt tct tcc 595
Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser
                        150                        155                        160                        165

ggc aag ggc caa tct gtt ttg cgt agt tca gac gat ctg cag gca gca 643
Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala
                        170                        175                        180

tgg gat tat gcg atg agc ggt gca cgc gtg gcc aac tcc cgc gtc atc 691

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Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala	Asn	Ser	Arg	Val	Ile		
			185					190					195				
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Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	Thr	Leu	Leu	Thr	Val		
		200					205					210					
agg	tcc	atc	gat	ccc	acc	acc	tct	aag	cct	gcg	acc	tgg	ttc	tgt	gag	787	
Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	Thr	Trp	Phe	Cys	Glu		
	215					220					225						
ccc	att	ggg	cac	cgc	caa	gaa	gac	ggc	gac	tac	gtg	gaa	tcc	tgg	cag	835	
Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	Val	Glu	Ser	Trp	Gln		
230					235					240					245		
cca	atg	gag	atg	act	cct	cgc	gcg	ctg	gaa	aac	gca	cgc	tca	gta	gcc	883	
Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Ser	Val	Ala		
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1123																	
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gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	gca	gtg	gct	gaa		
1171																	
Glu	Gly	Val	Ser	Tyr	Thr	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Val	Ala	Glu		
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act	gat	ctt	cgt	atc	ttt	gcc	aag	cca	gag	gcc	ttc	acc	aag	cgt	cgc		
1219																	
Thr	Asp	Leu	Arg	Ile	Phe	Ala	Lys	Pro	Glu	Ala	Phe	Thr	Lys	Arg	Arg		
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atg	ggg	gtt	gca	gtg	tcc	acc	gct	gag	gat	gtg	gct	gca	gcc	agg	gac		
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Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp		
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                   20                  25                  30  
 Ala Phe Gln Arg Leu Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu  
           35                  40                  45  
 His Ala Pro Ala His Gln Val Ala His Phe Ser Tyr Val Ile Asp Met  
   50                  55                  60  
 Thr Asp Ala Ala Gln Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp  
   65                  70                  75                  80  
 Phe Val Ile Pro Glu Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys  
                   85                  90                  95  
 Ile Glu Glu Glu Gly Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala  
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 Lys Leu Thr Met Asn Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu  
   115                  120                  125  
 Leu Gly Leu Pro Thr Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu  
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 Phe Ser Ala Ala Ala Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro  
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 Val Met Ser Ser Ser Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp  
                   165                  170                  175  
 Asp Leu Gln Ala Ala Trp Asp Tyr Ala Met Ser Gly Ala Arg Val Ala  
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 Asn Ser Arg Val Ile Val Glu Ala Phe Val Glu Phe Asp Tyr Glu Ile  
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 Thr Leu Leu Thr Val Arg Ser Ile Asp Pro Thr Thr Ser Lys Pro Ala  
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 Thr Trp Phe Cys Glu Pro Ile Gly His Arg Gln Glu Asp Gly Asp Tyr  
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 Val Glu Ser Trp Gln Pro Met Glu Met Thr Pro Arg Ala Leu Glu Asn  
           245                  250                  255

Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly  
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Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser  
 275 280 285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr  
 290 295 300

Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu  
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Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr  
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Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala  
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Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala  
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Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val  
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 Met Ser Thr Phe Val  
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 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro  
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 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu  
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259  
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val  
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307



Met	Trp	Ser	Glu	His	Cys	Ser	Tyr	Lys	Ser	Ser	Lys	Val	His	Leu	Arg	
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Tyr	Phe	Gly	Glu	Thr	Thr	Thr	Glu	Glu	Met	Ala	Ser	Lys	Ile	Leu	Ala	
70					75				80						85	
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Gly	Ile	Gly	Glu	Asn	Ala	Gly	Val	Val	Asp	Ile	Gly	Asp	Gly	Asn	Ala	
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gtg	acc	ttc	cgc	gtg	gag	tcc	cac	aac	cac	cca	tcc	ttc	gta	gag	cca	451
Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro	
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His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met	
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gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggt	547
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly	
	135					140					145					
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Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp	
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ggc	att	tcc	cat	tac	ggc	aac	tgc	ctc	ggc	ctg	cca	aac	atc	ggt	ggc	643
Gly	Ile	Ser	His		Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly	
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gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggg	aac	cca	ctg	gtc	aac	gca	691
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala	
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Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala	
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Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu	
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Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu	
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Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala	
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gag	aag	gta	ctc	atc	gag	tgc	tgc	ctc	gag	ctg	tac	aag	gct	ggc	gtc	931
Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val	
			265					270					275			
gtg	gtc	ggg	att	cag	gac	ctc	ggg	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr	
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tct	gag	ctg	gca	gcc	gca	ggc	gac	ggc	ggc	atg	cgc	gtc	aac	cta	gac	1027

Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met Arg Val Asn Leu Asp  
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 Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala  
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 Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val  
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 gag cgt ttc ctc gag atc tgt gca aag tgg gat gtc acc tgc gca gaa  
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 Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu  
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 Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln  
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 Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala  
 440 445 450  
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 Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg  
 455 460 465  
 ggc gtt gcg atc tcc gcc gac gca tcc ggc cgt tac acc aag ctc gag  
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 Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu  
 470 475 480 485  
 cca aac act ggc gcg cag ctt gca ctg gct gag gct tac cgc aac gtg  
 1603  
 Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

490	495	500
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Val Ser Thr	Gly Ala Arg Pro Val	Ala Val Thr Asn Cys Leu Asn Phe
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1699		
Gly Ser Pro	Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu Ala Val	
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cac ggt ctg gca gac gga tcc aag ctt ttg ggc att cca gtg tcc ggc		
1747		
His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val Ser Gly		
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ggg aac gtc tcc ttc tac aac cag act ggt gac gag ccc atc ctg cca		
1795		
Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile Leu Pro		
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1843		
Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu Gln Ser		
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atc ggc aac gtc ctc cca tcc gag gac aac gat ctc tac ctc ctg ggt		
1891		
Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu Leu Gly		
	585	590 595
gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc		
1939		
Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val Ser Gly		
	600	605 610
gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag		
1987		
Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn Glu Gln		
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cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac		
2035		
Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala Ser His		
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gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc		
2083		
Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu Ala Ile		
	650	655 660
cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc		
2131		
His Gln Lys Lys Gly Met Asp Val Asp Leu Ser Gln Ile His Pro Ser		
	665	670 675
ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca		
2179		
Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser Arg Ile Val Val Ala		
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acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt  
2227

Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val  
695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc  
2275

Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val  
710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa  
2323

Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu  
730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct  
2371

Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala  
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Asn Ala Val Val Ala  
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<213> Corynebacterium glutamicum

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35 40 45

Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser  
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Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala  
65 70 75 80

Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile  
85 90 95

Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro  
100 105 110

Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile  
115 120 125

Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp  
130 135 140

Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe

145	150	155	160
Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu	165	170	175
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn	180	185	190
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu	195	200	205
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly	210	215	220
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser	225	230	235
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val	245	250	255
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu	260	265	270
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly	275	280	285
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met	290	295	300
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala	305	310	315
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val	325	330	335
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp	340	345	350
Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr	355	360	365
Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr	370	375	380
Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn	385	390	395
Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val	405	410	415
Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu	420	425	430
Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly	435	440	445
Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp	450	455	460
Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg	465	470	475
			480

Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu  
 485 490 495  
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr  
 500 505 510  
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln  
 515 520 525  
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly  
 530 535 540  
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp  
 545 550 555 560  
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp  
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 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp  
 580 585 590  
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp  
 595 600 605  
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp  
 610 615 620  
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu  
 625 630 635 640  
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu  
 645 650 655  
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser  
 660 665 670  
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser  
 675 680 685  
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala  
 690 695 700  
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 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val  
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&lt;211&gt; 638

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

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&lt;222&gt; (54) .. (638)

&lt;223&gt; FRXA02805

&lt;400&gt; 913

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Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
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Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
      20                      25                      30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
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Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
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Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
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gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
      85                      90                      95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
     100                      105                      110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
    115                      120                      125                      130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
      135                      140                      145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
      150                      155                      160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
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acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
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gtc
Val
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 <213> Corynebacterium glutamicum

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 Val Phe Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu  
   1                  5                  10                  15  
 Gly Leu Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala  
                   20                  25                  30  
 Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu  
                   35                  40                  45  
 Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu  
                   50                  55                  60  
 Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu  
   65                  70                  75                  80  
 Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val  
                   85                  90                  95  
 Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu  
                   100                  105                  110  
 Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly  
                   115                  120                  125  
 Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly  
                   130                  135                  140  
 Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met  
   145                  150                  155                  160  
 Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala  
                   165                  170                  175  
 Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys  
                   180                  185                  190  
 Trp Asp Val  
                   195

<210> 915  
 <211> 697  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (23)..(697)  
 <223> FRXA00537

<400> 915  
 caacagcact tgcattccgc gcgtg tat cac cga gca gta ctg aac gct acg   52  
                   Val Tyr His Arg Ala Val Leu Asn Ala Thr



<210> 916  
<211> 225

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 916

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Val Tyr His Arg Ala Val Leu Asn Ala Thr Ser Ala Ala Thr Pro Phe
 1           5           10           15

Lys Gln Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr
          20           25           30

Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys
          35           40           45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg
 50           55           60

Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu
 65           70           75           80

Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu
          85           90           95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val
          100          105          110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile
          115          120          125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu
          130          135          140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu
          145          150          155          160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val
          165          170          175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn
          180          185          190

Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala
          195          200          205

Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu
          210          215          220

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Ala

225

&lt;210&gt; 917

&lt;211&gt; 302

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (279)

&lt;223&gt; FRXA00561

&lt;400&gt; 917

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ctc ttc cca gat cca ccc atc cct gtt cac ctc act tgt ttg ctg agt 48
Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
 1                    5                    10                    15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa 96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
      20                    25                    30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc 144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
      35                    40                    45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act 192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
      50                    55                    60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag 240
Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
      65                    70                    75                    80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg 289
Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
      85                    90

ctgtgaagcc ggg 302

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<210> 918  
 <211> 93  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
 1                    5                    10                    15

Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
      20                    25                    30

Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
      35                    40                    45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
      50                    55                    60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
      65                    70                    75                    80

Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
      85                    90

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<210> 919  
 <211> 792  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(769)  
 <223> RXA00541

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tcacgaaga cttcgatgtg gtgggagttg aggtcgcgaa gtg agc gcc aaa atc 115
                               Val Ser Ala Lys Ile
                               1           5

ggt gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163
Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg
                10                15                20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211
Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp
                25                30                35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259
Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser
                40                45                50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307
Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val
                55                60                65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355
Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly
                70                75                80                85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403
Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly
                90                95                100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451
Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His
                105                110                115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499
Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys
                120                125                130

ggt cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547
Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln
                135                140                145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595
Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val
                150                155                160                165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643
Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly
                170                175                180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691
Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu
                185                190                195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739
His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu
                200                205                210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789

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Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
215 220

act

792

<210> 920

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 920

Val Ser Ala Lys Ile Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp  
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Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser  
20 25 30

Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val  
35 40 45

Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser  
50 55 60

Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly  
65 70 75 80

Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala  
85 90 95

Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His  
100 105 110

Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr  
115 120 125

Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly  
130 135 140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly  
145 150 155 160

Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val  
165 170 175

Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu  
180 185 190

Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile  
195 200 205

Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
210 215 220

<210> 921

<211> 1014

<212> DNA

<213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)..(991)

&lt;223&gt; RXA00620

&lt;400&gt; 921

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aattttccga acacacccga ggggtctaga cttgcctaac atg cgt cct gaa ctc 115
                                         Met Arg Pro Glu Leu
                                         1 5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
              10              15              20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
              25              30              35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
              40              45              50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
              55              60              65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
              70              75              80              85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
              90              95              100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
              105              110              115

agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
              120              125              130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
              135              140              145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
              150              155              160              165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
              170              175              180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
              185              190              195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

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200	205	210	
gaa gtc ctt acc cca gat tcc tcc cgc tac tgg cct ttg gaa ggc tat			787
Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr			
215	220	225	
gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac			835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
250	255		260
cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
265	270		275
atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
280	285		290
ggt tct tgc gtc taagctgctt gattttccct aaa			
1014			
Gly Ser Cys Val			
295			
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<211> 297			
<212> PRT			
<213> Corynebacterium glutamicum			
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Met Arg Pro Glu Leu Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val			
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Arg Glu Ile Tyr Glu Ile Asp Asp Lys His Ile Leu Met Val Ala Ser			
20	25		30
Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp			
35	40		45
Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile			
50	55		60
Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro			
65	70	75	80
Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu			
85	90		95
Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val			
100	105		110
Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly			
115	120		125
Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr			
130	135		140

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val  
 145 150 155 160  
 Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser  
 165 170 175  
 Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val  
 180 185 190  
 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr  
 195 200 205  
 Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp  
 210 215 220  
 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys  
 225 230 235 240  
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys  
 245 250 255  
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala  
 260 265 270  
 Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys  
 275 280 285  
 Phe Cys Gln Trp Ile Gly Ser Cys Val  
 290 295

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 <223> RXN00770

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 cctcaagtta agatcggttag gcgatagggg ttgagcattt ttg ctc tcc ccg tat 115  
 Leu Leu Ser Pro Tyr  
 1 5  
 gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163  
 Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys  
 10 15 20  
 ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211  
 Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln  
 25 30 35  
 gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259  
 Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile  
 40 45 50  
 gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307



Glu	Ala	Gly	Asp	Arg	Ala	Val	Glu	Leu	Phe	Ala	Pro	Met	Ala	Lys	Arg		
55						60					65						
gcc	acc	cgc	cca	gag	gtt	ctt	ggc	aac	ctc	gga	ggc	ttc	gca	gga	ctc	355	
Ala	Thr	Arg	Pro	Glu	Val	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Ala	Gly	Leu		
70					75					80					85		
ttt	gag	ctc	gga	aaa	tac	aag	aag	cca	atc	ctc	gca	gca	gga	tct	gac	403	
Phe	Glu	Leu	Gly	Lys	Tyr	Lys	Lys	Pro	Ile	Leu	Ala	Ala	Gly	Ser	Asp		
				90					95					100			
gga	gtc	ggc	acc	aag	ctt	gtc	atc	gcc	cag	atg	atg	gac	aag	cac	gac	451	
Gly	Val	Gly	Thr	Lys	Leu	Val	Ile	Ala	Gln	Met	Met	Asp	Lys	His	Asp		
			105					110					115				
acc	atc	ggc	atc	gac	ctt	gtt	gca	atg	tgt	gtg	gat	gac	ctc	gtt	gtc	499	
Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	Asp	Asp	Leu	Val	Val		
	120						125					130					
acc	ggc	gca	gag	cca	ctg	ttc	ctc	cag	gac	tac	atc	gcc	atc	ggc	aag	547	
Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	Ile	Ala	Ile	Gly	Lys		
	135					140					145						
gtt	gtc	cca	gag	cac	gtt	gct	gag	atc	gtc	tcc	ggt	atc	gca	gaa	ggc	595	
Val	Val	Pro	Glu	His	Val	Ala	Glu	Ile	Val	Ser	Gly	Ile	Ala	Glu	Gly		
150					155					160					165		
tgt	gtc	cag	gca	ggc	tgt	gct	ctg	ctc	ggt	ggc	gaa	acc	gca	gaa	cac	643	
Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	Glu	Thr	Ala	Glu	His		
				170					175					180			
cca	ggt	gtt	atg	gaa	cca	gac	cac	tac	gat	gtc	tcc	gca	act	gca	gtc	691	
Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	Ser	Ala	Thr	Ala	Val		
			185					190					195				
ggc	gtt	gtc	gaa	gca	gat	gaa	ctg	cta	gga	cca	gac	cgc	gtc	cgc	gca	739	
Gly	Val	Val	Glu	Ala	Asp	Glu	Leu	Leu	Gly	Pro	Asp	Arg	Val	Arg	Ala		
	200						205					210					
ggc	gac	gtc	ctc	atc	ggc	atg	gct	tcc	tcc	ggt	ctg	cac	tcc	aac	ggt	787	
Gly	Asp	Val	Leu	Ile	Gly	Met	Ala	Ser	Ser	Gly	Leu	His	Ser	Asn	Gly		
	215					220					225						
tac	tcc	ctg	gct	cgc	cac	gtc	ctc	ctg	gaa	aag	gca	ggc	ctg	gcg	ctt	835	
Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	Ala	Gly	Leu	Ala	Leu		
230					235					240					245		
gac	gga	cac	atc	gaa	gaa	ctc	gga	cgc	acc	ctc	ggt	gaa	gaa	ctt	ctc	883	
Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Glu	Glu	Leu	Leu		
				250					255					260			
gag	cca	acc	cgc	atc	tac	gcc	aag	gac	tgc	ctg	gca	ctg	atc	gca	gag	931	
Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	Ala	Leu	Ile	Ala	Glu		
			265					270					275				
tgc	gaa	gtt	cac	acc	ttc	tgc	cac	gtc	acc	ggc	ggc	ggc	ctc	gca	ggc	979	
Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	Gly	Gly	Leu	Ala	Gly		
	280						285						290				
aac	ctc	gag	cgg	gtt	gtc	cca	gaa	ggg	ctc	gtc	gca	gaa	atg	tcc	cga	1027	

Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg  
 295 300 305  
 gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc  
 1075  
 Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly  
 310 315 320 325  
 aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc  
 1123  
 Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly  
 330 335 340  
 atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg  
 1171  
 Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met  
 345 350 355  
 ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac  
 1219  
 Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn  
 360 365 370  
 ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc  
 1267  
 Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn Gly Glu His Pro Gly  
 375 380 385  
 tac taagcccaac tgtctgctct aag  
 1293  
 Tyr  
 390

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 Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr  
 20 25 30  
 Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
 35 40 45  
 Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
 50 55 60  
 Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
 65 70 75 80  
 Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
 85 90 95  
 Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
 115 120 125  
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
 130 135 140  
 Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
 145 150 155 160  
 Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
 165 170 175  
 Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
 180 185 190  
 Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
 195 200 205  
 Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
 210 215 220  
 Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
 225 230 235 240  
 Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu  
 245 250 255  
 Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu  
 260 265 270  
 Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly  
 275 280 285  
 Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val  
 290 295 300  
 Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr  
 305 310 315 320  
 Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe  
 325 330 335  
 Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp  
 340 345 350  
 Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile  
 355 360 365  
 Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn  
 370 375 380  
 Gly Glu His Pro Gly Tyr  
 385 390

&lt;210&gt; 925

&lt;211&gt; 818

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15)..(818)

&lt;223&gt; FRXA00557

&lt;400&gt; 925

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tgggttgagc atttttg ctc tcc ccg tat gcg tgg ggg ttg tcc cgc gca    50
      Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala
        1              5              10

ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa    98
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu
      15              20              25

gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt    146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val
      30              35              40

tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc    194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val
      45              50              55              60

gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt    242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu
      65              70              75

ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag    290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys
      80              85              90

aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc    338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val
      95              100              105

atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt    386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val
      110              115              120

gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc    434
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe
      125              130              135              140

ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct    482
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala
      145              150              155

gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct    530
Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala
      160              165              170

ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac    578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp
      175              180              185

cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa    626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu
      190              195              200

ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg    674
Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met
      205              210              215              220

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gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722  
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val  
                   225                                  230                                  235

ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770  
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu  
                   240                                  245                                  250

gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818  
 Gly Arg Thr Pro Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala  
                   255                                  260                                  265

<210> 926

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 926

Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser  
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Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr  
                   20                                  25                                  30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
                   35                                  40                                  45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
                   50                                  55                                  60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
                   65                                  70                                  75                                  80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
                   85                                  90                                  95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
                   100                                  105                                  110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
                   115                                  120                                  125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
                   130                                  135                                  140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
                   145                                  150                                  155                                  160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
                   165                                  170                                  175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
                   180                                  185                                  190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
                   195                                  200                                  205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
                   210                                  215                                  220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro  
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala  
 260 265

<210> 927

<211> 338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

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 Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu  
 1 5 10 15

ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96  
 Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile  
 20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144  
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu  
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192  
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys  
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240  
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys  
 65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288  
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val  
 85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgctct 335  
 Ile Leu Asn Gly Glu His Pro Gly Tyr  
 100 105

aag 338

<210> 928

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 928

Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu  
 1 5 10 15

Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile  
                   20                  25                  30  
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu  
           35                  40                  45  
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys  
       50                  55                  60  
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys  
   65                  70                  75                  80  
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val  
                   85                  90                  95  
 Ile Leu Asn Gly Glu His Pro Gly Tyr  
           100                  105

&lt;210&gt; 929

&lt;211&gt; 1320

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1297)

&lt;223&gt; RXN02345

&lt;400&gt; 929

accaccgacc ctatgtaatc aaccagggttc ccaaggctcg aaaagtggaa gcgctgctca 60  
 aagatcttac attttgggtga aggcgttata gttaggactt gtg act tct aca gga 115  
   Val Thr Ser Thr Gly  
   1                  5  
 aac caa gcc cac gct cca gga atg ccc atc gtc gca gta att ggt gac 163  
 Asn Gln Ala His Ala Pro Gly Met Pro Ile Val Ala Val Ile Gly Asp  
                   10                  15                  20  
 ggc caa tta gcc cgc atg atg cag acc tcc gcc atc gaa ctc gga caa 211  
 Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala Ile Glu Leu Gly Gln  
                   25                  30                  35  
 tca ctg cga gtt cta gct gga gcg ccg gat tcc tcc gca gct caa gta 259  
 Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser Ser Ala Ala Gln Val  
                   40                  45                  50  
 gct gct gat gtt gtt ctc ggc gat tac acc aac att gat gat ctg cgc 307  
 Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn Ile Asp Asp Leu Arg  
                   55                  60                  65  
 gtc gcc atc gaa ggc gcc gat gtg atg acc ttc gac cac gag cac gtc 355  
 Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe Asp His Glu His Val  
                   70                  75                  80                  85  
 ccc aac gaa cac ctg cac caa ctc atc gca gaa ggc gtc aac gtt cag 403  
 Pro Asn Glu His Leu His Gln Leu Ile Ala Glu Gly Val Asn Val Gln  
                   90                  95                  100  
 cca cgc cca gaa gcg ctg gtc aac gca caa gac aaa ctt gtc atg cgc 451

Pro	Arg	Pro	Glu	Ala	Leu	Val	Asn	Ala	Gln	Asp	Lys	Leu	Val	Met	Arg	
			105					110					115			
aag	cgt	cta	cgt	gaa	ctc	ggc	gca	cca	gtc	cca	cca	ttt	gct	gcc	att	499
Lys	Arg	Leu	Arg	Glu	Leu	Gly	Ala	Pro	Val	Pro	Pro	Phe	Ala	Ala	Ile	
		120					125					130				
gaa	tca	gtc	gaa	gat	gca	gtg	gga	ttc	ttc	gaa	gca	gtt	gat	ggc	caa	547
Glu	Ser	Val	Glu	Asp	Ala	Val	Gly	Phe	Phe	Glu	Ala	Val	Asp	Gly	Gln	
		135				140					145					
gtt	tgc	ctc	aaa	gca	cgc	cgt	ggc	gga	tac	gac	ggc	aag	ggc	gta	tgg	595
Val	Cys	Leu	Lys	Ala	Arg	Arg	Gly	Gly	Tyr	Asp	Gly	Lys	Gly	Val	Trp	
150					155					160					165	
ttc	cca	gcc	gat	gta	gca	gag	ctt	cag	tcg	ctt	gtg	gca	gag	ctt	ctc	643
Phe	Pro	Ala	Asp	Val	Ala	Glu	Leu	Gln	Ser	Leu	Val	Ala	Glu	Leu	Leu	
				170				175						180		
gac	ggc	ggc	acc	cca	ctc	atg	gca	gaa	aag	aaa	gtt	gcc	ctc	aac	agg	691
Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val	Ala	Leu	Asn	Arg	
			185					190					195			
gaa	ctg	tcc	gcc	atg	gtt	gcc	cgc	acc	cca	agt	gga	gaa	acc	aaa	gcg	739
Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly	Glu	Thr	Lys	Ala	
		200					205					210				
tgg	cca	gtc	gta	gaa	tca	gtg	cag	aag	aac	ggg	gtg	tgt	gca	gaa	gca	787
Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val	Cys	Ala	Glu	Ala	
	215					220					225					
atc	gct	ccc	gca	cct	gaa	cta	tcc	gca	gaa	ctg	cag	gaa	tcc	acc	aga	835
Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln	Glu	Ser	Thr	Arg	
230					235					240					245	
gga	ttg	gcc	cag	aag	atc	gcc	acg	gaa	ctc	ggc	gtc	act	ggg	gtc	ttg	883
Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val	Thr	Gly	Val	Leu	
			250					255						260		
gca	gtg	gag	ctt	ttt	gaa	acc	ctc	gac	caa	aac	ggg	cag	cca	gag	atc	931
Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly	Gln	Pro	Glu	Ile	
			265					270					275			
ttt	gtc	aac	gag	ctc	gcc	atg	cgt	tca	cac	aac	acc	ggc	cac	tgg	act	979
Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr	Gly	His	Trp	Thr	
		280					285					290				
caa	gat	ggc	tgc	gtg	acc	agc	caa	ttc	gag	cag	cac	ctc	cgc	gca	gtc	
1027																
Gln	Asp	Gly	Cys	Val	Thr	Ser	Gln	Phe	Glu	Gln	His	Leu	Arg	Ala	Val	
		295				300					305					
ctc	gac	tac	cca	ctg	ggg	gct	acc	gac	act	ttg	gct	gat	tac	acc	gtg	
1075																
Leu	Asp	Tyr	Pro	Leu	Gly	Ala	Thr	Asp	Thr	Leu	Ala	Asp	Tyr	Thr	Val	
310					315					320					325	
atg	gcc	aac	gtg	ctc	ggg	gcc	gac	acc	gac	cca	gag	atg	ccc	atg	gca	
1123																
Met	Ala	Asn	Val	Leu	Gly	Ala	Asp	Thr	Asp	Pro	Glu	Met	Pro	Met	Ala	
			330						335					340		



acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac  
 1171  
 Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His  
 345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac  
 1219  
 Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn  
 360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc  
 1267  
 Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys  
 375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta  
 1317  
 Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
 390 395

gca  
 1320

<210> 930

<211> 399

<212> PRT

<213> Corynebacterium glutamicum

<400> 930

Val Thr Ser Thr Gly Asn Gln Ala His Ala Pro Gly Met Pro Ile Val  
 1 5 10 15

Ala Val Ile Gly Asp Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala  
 20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser  
 35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn  
 50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe  
 65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu  
 85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp  
 100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro  
 115 120 125

Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu  
 130 135 140

Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp  
 145 150 155 160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu  
 165 170 175  
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys  
 180 185 190  
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser  
 195 200 205  
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly  
 210 215 220  
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu  
 225 230 235 240  
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly  
 245 250 255  
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn  
 260 265 270  
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn  
 275 280 285  
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln  
 290 295 300  
 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu  
 305 310 315 320  
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro  
 325 330 335  
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro  
 340 345 350  
 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys  
 355 360 365  
 Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala  
 370 375 380  
 Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
 385 390 395

&lt;210&gt; 931

&lt;211&gt; 833

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(810)

&lt;223&gt; FRXA02345

&lt;400&gt; 931

ttt gct gcc att gaa tca gtc gaa gat gca gtg gga ttc ttc gaa gca 48  
 Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala  
 1 5 10 15

gtt gat ggc caa gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	96
20 25 30	
aag ggc gta tgg ttc cca gcc gat gta gca gag ctt cag tcg ctt gtg Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	144
35 40 45	
gca gag ctt ctc gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	192
50 55 60	
gcc ctc aac agg gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	240
65 70 75 80	
gaa acc aaa gcg tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	288
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	336
100 105 110	
gaa tcc acc aga gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	384
115 120 125	
act ggt gtc ttg gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	432
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	480
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	528
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	576
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	624
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	672
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	720
225 230 235 240	
ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu	768
245 250 255	
gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat	810

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
                   260                                  265                                  270

taggtctttt ctgagcgcta gca

833

<210> 932

<211> 270

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 932

Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala  
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Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly  
                   20                                  25                                  30

Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val  
           35                                  40                                  45

Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val  
   50                                  55                                  60

Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly  
   65                                  70                                  75                                  80

Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val  
                   85                                  90                                  95

Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln  
                   100                                  105                                  110

Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val  
           115                                  120                                  125

Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly  
   130                                  135                                  140

Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr  
   145                                  150                                  155                                  160

Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His  
                   165                                  170                                  175

Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala  
                   180                                  185                                  190

Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu  
           195                                  200                                  205

Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp  
   210                                  215                                  220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile  
   225                                  230                                  235                                  240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu  
                   245                                  250                                  255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp

260

265

270

<210> 933  
 <211> 618  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(595)  
 <223> RXN02350

&lt;400&gt; 933

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ataaaccgat acgtactttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115
                                   Val Gly Pro Leu Val
                                   1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala
              10              15              20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val
              25              30              35

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259
Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala
              40              45              50

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307
His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala
              55              60              65

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355
His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly
              70              75              80              85

gtt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403
Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser
              90              95              100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451
Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly
              105              110              115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499
Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly
              120              125              130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547
Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala
              135              140              145

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595
Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
              150              155              160              165

taatgaatcc gatcgtggtg ctg 618

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<210> 934
<211> 165
<212> PRT
<213> Corynebacterium glutamicum
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<400> 934
Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp
  1          5          10          15
Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
          20          25          30
Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn
          35          40          45
Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys
          50          55          60
Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro
          65          70          75          80
Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu
          85          90          95
Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala
          100          105          110
Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg
          115          120          125
Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr
          130          135          140
Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys
          145          150          155          160
Lys Arg Leu Leu Gly
          165

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<210> 935
<211> 223
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(223)  
<223> FRXA02346
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<400> 935
aagcatttct ccaacacttt tgatggacag attaacgctt aaaaggcctg ttatagactg 60
ataaaaccgat acgtaacttt cgcgccttaag gagaatttca gtg ggt cct cta gtt    115
                                     Val Gly Pro Leu Val
                                     1                               5
ggg ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct    163
Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala

```

	10	15	20	
gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc				211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val				
	25	30	35	
tct gca cac cgc				223
Ser Ala His Arg				
	40			
<210> 936				
<211> 41				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 936				
Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp				
1 5 10 15				
Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe				
	20	25	30	
Glu Val Gly Val Val Ser Ala His Arg				
	35	40		
<210> 937				
<211> 252				
<212> DNA				
<213> Corynebacterium glutamicum				
<220>				
<221> CDS				
<222> (20)..(229)				
<223> FRXA02350				
<400> 937				
atactaggat ctcgacggtttg gat tcc ttg ctg tcc atc gtc cag atg cca				52
	Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro			
	1 5 10			
ggc ggc gtt cca gtc gcc act gtc tcc atc ggt ggc gcg aag aat gca				100
Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala				
	15 20 25			
ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc				148
Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val				
	30 35 40			
acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc				196
Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala				
	45 50 55			
aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtggtg				249
Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly				
	60 65 70			
ctg				252

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<210> 938
<211> 70
<212> PRT
<213> Corynebacterium glutamicum
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<400> 938
Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val
 1             5             10             15
Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val
      20             25             30
Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp
      35             40             45
Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu
      50             55             60
Lys Lys Arg Leu Leu Gly
      65             70

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<210> 939
<211> 999
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(976)  
<223> RXA01087
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<400> 939																
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tatctcta				at	ccaaactgca	cctatatata	aggagtaaaa	atg	caa	acc	ctt	gct				115
								Met	Gln	Thr	Leu	Ala				
								1				5				
gct att gtt	cgt gcc acg	aag caa cct	ttt gag atc	acc acc att	gat											163
Ala Ile Val	Arg Ala Thr	Lys Gln Pro	Phe Glu Ile	Thr Thr Ile	Asp											
				10					15					20		
ctg gat gca	cca cga cca	gat gaa gtt	caa atc cgt	gtt att gct	gcc											211
Leu Asp Ala	Pro Arg Pro	Asp Glu Val	Gln Ile Arg	Val Ile Ala	Ala											
				25					30					35		
gga gtg cgc	cac act gac	gca att gtt	cgt gat cag	att tac cca	act											259
Gly Val Arg	His Thr Asp	Ala Ile Val	Arg Asp Gln	Ile Tyr Pro	Thr											
				40					45					50		
ttt ctt ccc	gca gtt ttc	ggc cac gaa	ggc gcc gga	gta gtt gtc	gcc											307
Phe Leu Pro	Ala Val Phe	Gly His Glu	Gly Ala Gly	Val Val Val	Ala											
				55					60					65		
gtg ggt tct	gca gtc acc	tcg gtg aaa	cca gat gac	aag gta gtg	ctg											355
Val Gly Ser	Ala Val Thr	Ser Val Lys	Pro Asp Asp	Lys Val Val	Leu											
				70					75					80	85	
gga ttc aac	tct tgt ggc	cag tgc ttg	aag tgt ttg	ggc ggt aag	cct											403
Gly Phe Asn	Ser Cys Gly	Gln Cys Leu	Lys Cys Leu	Gly Gly Lys	Pro											



	90	95	100	
gcg tac tgt gag aaa ttc tat gac cgc aac ttc gca tgc acc cgc gat				451
Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe Ala Cys Thr Arg Asp				
	105	110	115	
gcc ggg cac act act ttg ttt acc cgt gca aca aaa gag cag gca gag				499
Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr Lys Glu Gln Ala Glu				
	120	125	130	
gcc atc atc gac acc ctt gat gat gtt ttc tac gat gcg gat gcg ggt				547
Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr Asp Ala Asp Ala Gly				
	135	140	145	
ttc ctg gca tac cca gca act ccc cca gag gct tcg gga gta agc gtg				595
Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala Ser Gly Val Ser Val				
	150	155	160	165
ttg gtt gtc gcg gct ggt acc tct gat ctc ccc caa gca aag gaa gca				643
Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro Gln Ala Lys Glu Ala				
	170	175	180	
cta cac act gcc tcc tac ttg ggg cgc tcc acc tca ctg att gtt gat				691
Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr Ser Leu Ile Val Asp				
	185	190	195	
ttt gga gtg gct ggc atc cac cgc ctg ctt tca tac gaa gaa gaa ctc				739
Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser Tyr Glu Glu Glu Leu				
	200	205	210	
cgc gct gcg ggc gtg ctc atc gtt gcc gct gga atg gat ggt gcg cta				787
Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly Met Asp Gly Ala Leu				
	215	220	225	
ccc gga gtt gtc gca ggc tta gtg tcc gca cct gtc gtc gca ctg cca				835
Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro Val Val Ala Leu Pro				
	230	235	240	245
acc tcc gtg gga tac ggc gca ggt gct gga gga atc gca cca ctt ctg				883
Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly Ile Ala Pro Leu Leu				
	250	255	260	
acc atg ctt aac gcc tgc gcg ccg gga gtt gga gtg gtc aac att gat				931
Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly Val Val Asn Ile Asp				
	265	270	275	
aac ggc tat gga gca gga cac ctg gct gcg cag att gcg gcg agg				976
Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln Ile Ala Ala Arg				
	280	285	290	
taagggtttc gcaggagacg aac				999

&lt;210&gt; 940

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 940

Met	Gln	Thr	Leu	Ala	Ala	Ile	Val	Arg	Ala	Thr	Lys	Gln	Pro	Phe	Glu
1					5				10						15

Ile Thr Thr Ile Asp Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile  
 20 25 30  
 Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp  
 35 40 45  
 Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala  
 50 55 60  
 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp  
 65 70 75 80  
 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys  
 85 90 95  
 Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe  
 100 105 110  
 Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr  
 115 120 125  
 Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr  
 130 135 140  
 Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala  
 145 150 155 160  
 Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro  
 165 170 175  
 Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr  
 180 185 190  
 Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser  
 195 200 205  
 Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly  
 210 215 220  
 Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro  
 225 230 235 240  
 Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly  
 245 250 255  
 Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly  
 260 265 270  
 Val Val Asn Ile Asp Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln  
 275 280 285  
 Ile Ala Ala Arg  
 290

&lt;210&gt; 941

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXA00619

&lt;400&gt; 941

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tcaaaggaag acaccattga aggtgtgctgc aaaatcggag aattcatcaa aaaatagcag 60
cgactaggtt agtttcggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115
                                         Val Ala Asp Lys Lys
                                         1 5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
                10                15                20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
                25                30                35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
                40                45                50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
                55                60                65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
                70                75                80                85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
                90                95                100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
                105                110                115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
                120                125                130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
                135                140                145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
                150                155                160                165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
                170                175                180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
                185                190                195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

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Gln	Asp	Met	Leu	Asp	Leu	Met	Glu	Gly	Asp	Glu	Ala	Arg	Leu	Ser	Asp		
		200					205					210					
ctg	gaa	acc	cgc	atc	gca	gca	cac	ctc	ggc	ttt	gat	cgc	gtc	ttc	gac	787	
Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp		
	215					220					225						
tcc	gtc	ggc	cag	gtc	tac	cca	cgt	tcc	ctt	gac	ttc	gat	gca	gta	tct	835	
Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser		
	230				235					240					245		
gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883	
Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile		
				250					255					260			
cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggc	ttt	aag	gaa	ggc	931	
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly		
			265					270					275				
cag	gtc	ggc	tcc	tct	gca	atg	cct	cac	aag	atg	aac	gct	cgc	tcc	tgt	979	
Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys		
		280					285					290					
gag	cgc	gtg	ggc	ggc	ctg	cag	gtt	att	ctt	cgc	gga	tac	ctc	acc	atg		
	1027																
Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg	Gly	Tyr	Leu	Thr	Met		
	295					300					305						
gtt	gct	gat	ctt	tcc	ggc	cag	cag	tgg	aac	gaa	ggc	gat	gtc	ttc	tgc		
	1075																
Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys		
	310				315					320					325		
tcc	gtg	atc	cgc	cgc	gtt	gca	ctg	cca	gac	gca	ttc	ttc	gcg	att	gac		
	1123																
Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp		
				330					335					340			
gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggc	gca	ttc		
	1171																
Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp	Glu	Phe	Gly	Ala	Phe		
			345					350					355				
cct	gcc	atg	atc	gag	cgc	gaa	ctt	gag	cgt	tac	ctg	cca	ttc	ctg	gca		
	1219																
Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala		
		360					365					370					
act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa		
	1267																
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu		
		375				380					385						
acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gcg	gtt	gcc	ctc	aac		
	1315																
Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn		
	390				395					400					405		
atg	cgc	gaa	aat	ggc	ggc	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct		
	1363																
Met	Arg	Glu	Asn	Gly	Gly	Asp	Gln	Asp	Leu	Ile	Gln	Arg	Leu	Ala	Ala		

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                                410                                415                                420

gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct
1411
Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
      425                                430                                435

gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg
1459
Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
      440                                445                                450

ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac
1507
Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
      455                                460                                465

tac cga cca ggt gag att ctt taaaggtttt taacggcgtt cac
1551
Tyr Arg Pro Gly Glu Ile Leu
      470                                475

<210> 942
<211> 476
<212> PRT
<213> Corynebacterium glutamicum

<400> 942
Val Ala Asp Lys Lys Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala
  1              5              10              15

Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met
      20              25              30

Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
      35              40              45

Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
      50              55              60

Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
      65              70              75              80

Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
      85              90              95

His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
      100             105             110

Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
      115             120             125

Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
      130             135             140

Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
      145             150             155             160

Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
      165             170             175

```

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
 210 215 220  
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
 245 250 255  
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
 260 265 270  
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met  
 275 280 285  
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg  
 290 295 300  
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu  
 305 310 315 320  
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala  
 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
 340 345 350  
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
 355 360 365  
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala  
 370 375 380  
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val  
 385 390 395 400  
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile  
 405 410 415  
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu  
 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
 435 440 445  
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His  
 450 455 460  
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu  
 465 470 475

&lt;210&gt; 943

&lt;211&gt; 1683

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1660)

&lt;223&gt; RXA02622

&lt;400&gt; 943

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atcaagcagg ttgagcgtaa actcattgta gaagtcctga acagcgtgga attttcgctg 60

cagggtggcg tacaactcaa ctggagaggc taaatccttc atg agc gat gat cgt 115
                                   Met Ser Asp Asp Arg
                                   1      5

aag gca att aaa cgc gca cta att agc gtg tat gac aag act ggc ctg 163
Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
                                   10      15      20

gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
                                   25      30      35

acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
                                   40      45      50

ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
                                   55      60      65

aag aca ctg cac cct aag gtt cac gct ggc atc ttg gcg gac acc cgc 355
Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
                                   70      75      80      85

aag gaa gac cac ctg cgt cag ctc aag gaa ctt gag gtc gcc cca ttc 403
Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu Glu Val Ala Pro Phe
                                   90      95      100

cag ctt gtc gtg gtg aac ctg tac cca ttt gct gag acc gtt gcg tcc 451
Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala Glu Thr Val Ala Ser
                                   105      110      115

ggc gcc gat ttc gat gct tgc gtt gag cag atc gac atc gga ggc cca 499
Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
                                   120      125      130

tcc atg gtt cgt gct gcg gca aag aac cac cca tct gtc gct gtg gtt 547
Ser Met Val Arg Ala Ala Ala Lys Asn His Pro Ser Val Ala Val Val
                                   135      140      145

gtt tca ccg aac cgc tac gag gat gtc cag gaa gct ttg aag acc ggt 595
Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu Ala Leu Lys Thr Gly
150      155      160      165

gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
                                   170      175      180

cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr Trp Met Ser Glu Gln

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185					190					195					
ctg gct gcc gaa gat tct gag act gag ttc cca ggt tgg atc ggc acc	739														
Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro Gly Trp Ile Gly Thr															
200 205 210															
acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag	787														
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln															
215 220 225															
tct gca gct ttg tac gtg ggc aac acc cgc gga ctt gca cag gct aag	835														
Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys															
230 235 240 245															
cag ttc cac ggc aag gaa atg agc tac aac aac tac acc gat tct gat	883														
Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn Tyr Thr Asp Ser Asp															
250 255 260															
gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc	931														
Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile															
265 270 275															
atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc	979														
Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile															
280 285 290															
gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc															
1027															
Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe															
295 300 305															
ggt ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac															
1075															
Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn															
310 315 320 325															
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa															
1123															
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu															
330 335 340															
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt															
1171															
Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu															
345 350 355															
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc															
1219															
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser															
360 365 370															
ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac															
1267															
Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp															
375 380 385															
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag															
1315															
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu															
390 395 400 405															



gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag  
1363

Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys  
410 415 420

tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc  
1411

Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly  
425 430 435

atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt  
1459

Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg  
440 445 450

gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc  
1507

Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe  
455 460 465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act  
1555

Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr  
470 475 480 485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag  
1603

Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu  
490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac  
1651

Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu Thr Gly Ala Arg His  
505 510 515

ttc gct cac taaagttttt aaagatttcg ctt  
1683

Phe Ala His  
520

<210> 944

<211> 520

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 944

Met Ser Asp Asp Arg Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr  
1 5 10 15

Asp Lys Thr Gly Leu Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn  
20 25 30

Val Glu Ile Val Ser Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu  
35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys  
50 55 60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile  
65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu  
                                     85                                    90                                    95  
 Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala  
                                     100                                    105                                    110  
 Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile  
                                     115                                    120                                    125  
 Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro  
                                     130                                    135                                    140  
 Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu  
                                     145                                    150                                    155                                    160  
 Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala  
                                     165                                    170                                    175  
 Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr  
                                     180                                    185                                    190  
 Trp Met Ser Glu Gln Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro  
                                     195                                    200                                    205  
 Gly Trp Ile Gly Thr Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly  
                                     210                                    215                                    220  
 Glu Asn Pro His Gln Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly  
                                     225                                    230                                    235                                    240  
 Leu Ala Gln Ala Lys Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn  
                                     245                                    250                                    255  
 Tyr Thr Asp Ser Asp Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg  
                                     260                                    265                                    270  
 Pro Cys Val Ala Ile Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val  
                                     275                                    280                                    285  
 Ser Asp Glu Ser Ile Ala Ala Ala His Arg Glu Ala His Ala Cys Asp  
                                     290                                    295                                    300  
 Ser Val Ser Ala Phe Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser  
                                     305                                    310                                    315                                    320  
 Val Glu Met Ala Asn Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile  
                                     325                                    330                                    335  
 Ala Pro Ser Tyr Glu Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys  
                                     340                                    345                                    350  
 Asn Ile Arg Ile Leu Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu  
                                     355                                    360                                    365  
 Ser Arg Glu Ile Ser Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile  
                                     370                                    375                                    380  
 His Ala Glu Gly Asp Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser  
                                     385                                    390                                    395                                    400

Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala  
 405 410 415

Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala  
 420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg  
 435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala  
 450 455 460

Ala Ser Asp Ala Phe Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala  
 465 470 475 480

Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp  
 485 490 495

Asn Glu Val Ile Glu Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu  
 500 505 510

Thr Gly Ala Arg His Phe Ala His  
 515 520

&lt;210&gt; 945

&lt;211&gt; 1641

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1618)

&lt;223&gt; RXN00488

&lt;400&gt; 945

gttgtggaat agcgtgtgag ctgcagcggg tatccgattt aaggacaagc tactaaagtt 60

tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115  
 Met Thr Thr Gln Ser  
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163  
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211  
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val  
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259  
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu  
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg  
 55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg  
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
150 155 160 165	
atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
gtt aag act gag cag cac ccg aac gca tcc aag gat gca tca ggt cgt	787
Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
gag gct gcg cag gcc atg att gaa gct ggc gca gac gct atc aag gtg	
1027	
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggt att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	
1075	
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	

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310                               315                               320                               325
ggt gca cct cag atc act gcg atc atg gag gca gct gtt cca gct cac
1123
Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His
                               330                               335                               340

aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt
1171
Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly
                               345                               350                               355

gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc
1219
Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly
                               360                               365                               370

tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc
1267
Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile
                               375                               380                               385

aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct
1315
Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala
390                               395                               400                               405

atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac
1363
Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp
                               410                               415                               420

cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa
1411
Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu
                               425                               430                               435

ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att
1459
Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile
                               440                               445                               450

cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc
1507
His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser
                               455                               460                               465

tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc
1555
Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser
470                               475                               480                               485

gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa
1603
Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu
                               490                               495                               500

gct cct aac tac cac tagattttgc tcacttaaag agc
1641
Ala Pro Asn Tyr His
                               505

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&lt;210&gt; 946

&lt;211&gt; 506

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 946

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys  
 1 5 10 15

Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp  
 20 25 30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr  
 35 40 45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr  
 50 55 60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile  
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val  
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr  
 100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg  
 115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val  
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg  
 145 150 155 160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu  
 165 170 175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val  
 180 185 190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile  
 195 200 205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys  
 210 215 220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu  
 225 230 235 240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile  
 245 250 255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met  
 260 265 270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly  
 275 280 285

Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala  
 290 295 300

Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg  
 305 310 315 320

Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala  
 325 330 335

Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly  
 340 345 350

Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn  
 355 360 365

Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly  
 370 375 380

Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met  
 385 390 395 400

Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg  
 405 410 415

Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp  
 420 425 430

Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro  
 435 440 445

Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met  
 450 455 460

Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe  
 465 470 475 480

Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile  
 485 490 495

Gln Gln Thr Val Glu Ala Pro Asn Tyr His  
 500 505

<210> 947

<211> 574

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (574)

<223> FRXA00492

<400> 947

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tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115  
 Met Thr Thr Gln Ser  
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163  
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
 10 15 20  
 tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211  
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val  
 25 30 35  
 cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259  
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu  
 40 45 50  
 aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg  
 55 60 65  
 atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg  
 70 75 80 85  
 aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403  
 Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg  
 90 95 100  
 tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451  
 Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met  
 105 110 115  
 agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499  
 Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly  
 120 125 130  
 ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547  
 Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn  
 135 140 145  
 cgc gat atg cgt ttt gaa agc gac atg 574  
 Arg Asp Met Arg Phe Glu Ser Asp Met  
 150 155

&lt;210&gt; 948

&lt;211&gt; 158

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 948

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys  
 1 5 10 15  
 Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp  
 20 25 30  
 Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr  
 35 40 45  
 Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr  
 50 55 60  
 Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile  
 65 70 75 80



Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val  
85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr  
100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg  
115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val  
130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met  
145 150 155

&lt;210&gt; 949

&lt;211&gt; 557

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(534)

&lt;223&gt; FRXA00488

&lt;400&gt; 949

cag atc act gcg atc atg gag gca gct gtt cca gct cac aag gct ggc	48
Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly	
1 5 10 15	
ggt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct	96
Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala	
20 25 30	
aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg	144
Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu	
35 40 45	
gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag	192
Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys	
50 55 60	
cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc	240
Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly	
65 70 75 80	
cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc	288
Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe	
85 90 95	
cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa	336
Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu	
100 105 110	
ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag	384
Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln	
115 120 125	
gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att	432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480  
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528  
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

tac cac tagattttgc tcacttaaagc agc 557  
 Tyr His

<210> 950  
 <211> 178  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 950  
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Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala  
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Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu  
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys  
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly  
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe  
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu  
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln  
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

Tyr His

<210> 951  
 <211> 1554

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1531)

&lt;223&gt; RXA02469

&lt;400&gt; 951

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cgtcgaaaag cagtagtaaa gcagcaggaa ggtggtggaa agagcaattg aggtaccctt 60

gccgtgttca gggataactg attaatcaac taggagaccc atg cgt ttt ctt aac 115
                               Met Arg Phe Leu Asn
                               1 5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163
Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val
                        10 15 20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211
Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr
                        25 30 35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259
Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr
                        40 45 50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307
Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly
                        55 60 65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355
Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr
                        70 75 80 85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc 403
Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr
                        90 95 100

gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag 451
Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys
                        105 110 115

cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc 499
Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly
                        120 125 130

atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg 547
Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val
                        135 140 145

ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc 595
Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser
                        150 155 160 165

ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc 643
Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala
                        170 175 180

ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc 691
Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr

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185	190	195	
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly 200 205 210			739
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly 215 220 225			787
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp 230 235 240 245			835
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile 250 255 260			883
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr 265 270 275			931
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys 280 285 290			979
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc 1027 Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly 295 300 305			
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc 1075 Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala 310 315 320 325			
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc 1123 Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro 330 335 340			
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc 1171 Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val 345 350 355			
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc 1219 Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe 360 365 370			
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg 1267 Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg 375 380 385			
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca 1315 Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala 390 395 400 405			

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att  
1363

Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile  
410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc  
1411

Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser  
425 430 435

ggc gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc  
1459

Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr  
440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca  
1507

Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala  
455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgttgt tgtgcctttg aga  
1554

Glu Gly Lys Pro Arg Ala Ser Arg  
470 475

<210> 952

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 952

Met Arg Phe Leu Asn Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser  
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Asp Val Phe Met Val Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser  
20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val  
35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile  
50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp  
65 70 75 80

Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe  
85 90 95

Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg  
100 105 110

Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly  
115 120 125

Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp  
130 135 140

Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu  
145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His  
 165 170 175  
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly  
 180 185 190  
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala  
 195 200 205  
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn  
 210 215 220  
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp  
 225 230 235 240  
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser  
 245 250 255  
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala  
 260 265 270  
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly  
 275 280 285  
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr  
 290 295 300  
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu  
 305 310 315 320  
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly  
 325 330 335  
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala  
 340 345 350  
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro  
 355 360 365  
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe  
 370 375 380  
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu  
 385 390 395 400  
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr  
 405 410 415  
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val  
 420 425 430  
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala  
 435 440 445  
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser  
 450 455 460  
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg  
 465 470 475

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<210> 953
<211> 1692
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1669)  
<223> RXN00487
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<400> 953																		
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agaatcttat ttggaggctc gtctagtaga gtgagttctt																		
										gtg	agc	ctt	cag	aca				115
										Val	Ser	Leu	Gln	Thr				
										1				5				
aat	cat	cgc	cca	gta	ctc	gtc	gtt	gac	ttc	ggc	gca	cag	tac	gcg	cag			163
Asn	His	Arg	Pro	Val	Leu	Val	Val	Asp	Phe	Gly	Ala	Gln	Tyr	Ala	Gln			
				10				15						20				
ctg	atc	gca	cgt	cgt	gtg	cgt	gag	gcc	ggc	atc	tac	tcc	gaa	gtc	atc			211
Leu	Ile	Ala	Arg	Arg	Val	Arg	Glu	Ala	Gly	Ile	Tyr	Ser	Glu	Val	Ile			
			25				30						35					
ccg	cac	acc	gcc	acc	gca	gac	gat	gtg	cgc	gct	aaa	aat	gca	gca	gcc			259
Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala	Lys	Asn	Ala	Ala	Ala			
		40				45					50							
ctc	gtc	ctt	tcc	ggg	ggc	cca	tcc	tcc	gtg	tat	gcc	gag	gga	gca	cca			307
Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr	Ala	Glu	Gly	Ala	Pro			
	55					60					65							
tcc	ctt	gac	gct	gag	att	ctt	gat	ctc	gga	ttg	cca	gta	ttt	ggc	att			355
Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu	Pro	Val	Phe	Gly	Ile			
70				75				80						85				
tgc	tac	ggc	ttc	caa	gcc	atg	acc	cac	gcg	ctt	ggg	ggc	acc	gtt	gcc			403
Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu	Gly	Gly	Thr	Val	Ala			
			90					95					100					
aac	acc	ggg	aag	cgc	gaa	tac	gga	cgc	acc	gac	atc	aac	gtt	gcc	ggg			451
Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp	Ile	Asn	Val	Ala	Gly			
			105				110					115						
ggc	gtc	ctc	cac	gaa	ggc	ctc	gaa	gcc	tgc	cac	aag	gtg	tgg	atg	agc			499
Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His	Lys	Val	Trp	Met	Ser			
	120					125					130							
cac	ggc	gac	gcc	gtc	tct	gaa	gcc	cca	gaa	ggg	ttc	gta	gtc	acc	gcg			547
His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly	Phe	Val	Val	Thr	Ala			
	135				140						145							
tcc	tcc	gaa	ggg	gcg														

cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027	
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	
tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt	
1075	
Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly	
310 315 320 325	
tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg	
1123	
Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val	
330 335 340	
gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac	
1171	
Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn	
345 350 355	
gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg	
1219	
Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu	
360 365 370	
cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc	
1267	
Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly	
375 380 385	
ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt	
1315	



Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
 390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
 1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
 1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
 1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
 440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg  
 1507

Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val  
 455 460 465

ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc  
 1555

Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg  
 470 475 480 485

ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa  
 1603

Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu  
 490 495 500

gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca  
 1651

Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro  
 505 510 515

gga acc atc gaa tgg gag taggccttaa atgagccttc gtt  
 1692

Gly Thr Ile Glu Trp Glu  
 520

<210> 954

<211> 523

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
 1 5 10 15

Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile  
 20 25 30

Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala  
 35 40 45

Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr  
 50 55 60

Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu  
 65 70 75 80  
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu  
 85 90 95  
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp  
 100 105 110  
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His  
 115 120 125  
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly  
 130 135 140  
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu  
 145 150 155 160  
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu  
 165 170 175  
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile  
 180 185 190  
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu  
 195 200 205  
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys  
 210 215 220  
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln  
 225 230 235 240  
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu  
 245 250 255  
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala  
 260 265 270  
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser  
 275 280 285  
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly  
 290 295 300  
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu  
 305 310 315 320  
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu  
 325 330 335  
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile  
 340 345 350  
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
 355 360 365  
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
 385 390 395 400  
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
 405 410 415  
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
 420 425 430  
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
 435 440 445  
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr  
 450 455 460  
 Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr  
 465 470 475 480  
 Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr  
 485 490 495  
 Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val  
 500 505 510  
 Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu  
 515 520

&lt;210&gt; 955

&lt;211&gt; 1486

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1486)

&lt;223&gt; FRXA00487

&lt;400&gt; 955

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 agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115  
 Val Ser Leu Gln Thr  
 1 5

 aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163  
 Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln  
 10 15 20

 ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211  
 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile  
 25 30 35

 ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259  
 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala  
 40 45 50

 ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307  
 Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro  
 55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027	
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt  
 1075  
 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly  
 310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg  
 1123  
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val  
 330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac  
 1171  
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn  
 345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg  
 1219  
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu  
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc  
 1267  
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly  
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt  
 1315  
 Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
 390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
 1363  
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
 1411  
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
 1459  
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
 440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc  
 1486  
 Ser Val Gly Val Gln Gly Asp Gly Arg  
 455 460

<210> 956

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
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Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile

20										25					30				
Tyr	Ser	Glu	Val	Ile	Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala				
		35					40					45							
Lys	Asn	Ala	Ala	Ala	Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr				
	50					55					60								
Ala	Glu	Gly	Ala	Pro	Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu				
	65				70					75					80				
Pro	Val	Phe	Gly	Ile	Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu				
				85					90					95					
Gly	Gly	Thr	Val	Ala	Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp				
			100					105					110						
Ile	Asn	Val	Ala	Gly	Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His				
		115					120					125							
Lys	Val	Trp	Met	Ser	His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly				
		130				135					140								
Phe	Val	Val	Thr	Ala	Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu				
	145				150					155					160				
Asn	Lys	Glu	Arg	Lys	Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu				
				165					170					175					
His	Ser	Pro	His	Gly	Gln	Ala	Val	Leu	Thr	Arg	Phe	Leu	Thr	Glu	Ile				
			180					185					190						
Ala	Gly	Leu	Glu	Gln	Asn	Trp	Thr	Ala	Ala	Asn	Ile	Ala	Glu	Glu	Leu				
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Ile	Glu	Lys	Val	Arg	Glu	Gln	Ile	Gly	Glu	Asp	Gly	Arg	Ala	Ile	Cys				
		210				215					220								
Gly	Leu	Ser	Gly	Gly	Val	Asp	Ser	Ala	Val	Ala	Gly	Ala	Leu	Val	Gln				
	225				230					235					240				
Arg	Ala	Ile	Gly	Asp	Arg	Leu	Thr	Cys	Val	Phe	Val	Asp	His	Gly	Leu				
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Leu	Arg	Ala	Gly	Glu	Arg	Glu	Gln	Val	Glu	Lys	Asp	Phe	Val	Ala	Ala				
			260					265						270					
Thr	Gly	Ala	Lys	Leu	Val	Thr	Val	Asp	Glu	Arg	Gln	Ala	Phe	Leu	Ser				
		275					280					285							
Lys	Leu	Ala	Gly	Val	Thr	Glu	Pro	Glu	Ala	Lys	Arg	Lys	Ala	Ile	Gly				
		290				295					300								
Ala	Glu	Phe	Ile	Arg	Ser	Phe	Glu	Arg	Ala	Val	Ala	Gly	Val	Leu	Glu				
	305				310					315					320				
Glu	Ala	Pro	Glu	Gly	Ser	Thr	Val	Asp	Phe	Leu	Val	Gln	Gly	Thr	Leu				
				325					330					335					
Tyr	Pro	Asp	Val	Val	Glu	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Ala	Asn	Ile				
			340					345						350					

Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
           355                                  360                                  365  
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
           370                                  375                                  380  
 Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
 385                                  390                                  395                                  400  
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
                                   405                                  410                                  415  
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
                                   420                                  425                                  430  
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
                                   435                                  440                                  445  
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg  
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<210> 957  
 <211> 693  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(670)  
 <223> RXA02237

<400> 957  
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 gcacttctcg agcgtttcgg cttcgaggat taattcttca gtg tcg ggc gat aac 115  
   Val Ser Gly Asp Asn  
   1                                  5  
 caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163  
 Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys  
                                   10                                  15                                  20  
 tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211  
 Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe  
                                   25                                  30                                  35  
 agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259  
 Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly  
                                   40                                  45                                  50  
 cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307  
 Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp  
                                   55                                  60                                  65  
 tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355  
 Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg  
           70                                  75                                  80                                  85  
 tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403

Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg  
                                   90                                  95                                  100  
 cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc 451  
 Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser  
                                   105                                  110                                  115  
 tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa 499  
 Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu  
                                   120                                  125                                  130  
 gtt ttg gtt gaa cgc ctc act gga cgt ggc acc gaa agc gaa gac gtt 547  
 Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr Glu Ser Glu Asp Val  
                                   135                                  140                                  145  
 att gct cgc agg ctc gag acc gca cgc gaa gaa ttg gct gct cag agc 595  
 Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu Leu Ala Ala Gln Ser  
 150                                  155                                  160                                  165  
 gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643  
 Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys  
                                   170                                  175                                  180  
 gct att gag gat gtt ctc ctc ggc gct tagccaaaac atagagcggc 690  
 Ala Ile Glu Asp Val Leu Leu Gly Ala  
                                   185                                  190  
 agg 693  
  
 <210> 958  
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 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 958  
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 Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val  
                                   20                                  25                                  30  
 Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro  
                                   35                                  40                                  45  
 Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe  
                                   50                                  55                                  60  
 Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His  
   65                                  70                                  75                                  80  
 Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala  
                                   85                                  90                                  95  
 Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala  
                                   100                                  105                                  110  
 Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala  
                                   115                                  120                                  125  
 Pro Pro Ser Trp Glu Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr



130		135		140
Glu Ser Glu Asp Val	Ile Ala Arg Arg	Leu Glu Thr Ala Arg	Glu Glu	
145	150	155	160	
Leu Ala Ala Gln Ser	Glu Phe Lys His	Val Ile Ile Asn Asp	Asp Val	
	165	170	175	
Asp Thr Ala Val Lys	Ala Ile Glu Asp	Val Leu Leu Gly	Ala	
	180	185	190	

&lt;210&gt; 959

&lt;211&gt; 1413

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1390)

&lt;223&gt; RXA01446

&lt;400&gt; 959

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tgcatactcc aacttcattg atcggatgtg acgtaaacca	atg gct gca atc gtt	115
	Met Ala Ala Ile Val	
	1 5	

att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat	163
Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp	
	10 15 20

att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac	211
Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn	
	25 30 35

aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag	259
Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys	
	40 45 50

ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc	307
Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly	
	55 60 65

aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc	355
Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly	
	70 75 80 85

ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac	403
Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn	
	90 95 100

gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa	451
Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu	
	105 110 115

cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc	499
Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly	
	120 125 130

cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547  
 Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp  
 135 140 145

att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595  
 Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp  
 150 155 160 165

tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643  
 Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val  
 170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc 691  
 Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg  
 185 190 195

ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag 739  
 Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln  
 200 205 210

ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg 787  
 Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val  
 215 220 225

gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt 835  
 Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly  
 230 235 240 245

ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc 883  
 Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser  
 250 255 260

ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc 931  
 Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe  
 265 270 275

cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt 979  
 Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly  
 280 285 290

ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac  
 1027  
 Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr  
 295 300 305

gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac  
 1075  
 Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp  
 310 315 320 325

tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca  
 1123  
 Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro  
 330 335 340

atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca  
 1171  
 Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro  
 345 350 355

ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg  
 1219  
 Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met  
           360                                  365                                  370

cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt  
 1267  
 Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu  
           375                                  380                                  385

cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt  
 1315  
 Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly  
           390                                  395                                  400                                  405

gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc  
 1363  
 Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile  
                                   410                                  415                                  420

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt  
 1410  
 Val Leu His Asp Val Leu Ala Asp Asn  
                                   425                                  430

gag  
 1413

<210> 960  
 <211> 430  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 960  
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                                   20                                  25                                  30  
 Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu  
                                   35                                  40                                  45  
 Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala  
                                   50                                  55                                  60  
 Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe  
   65                                  70                                  75                                  80  
 Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu  
                                   85                                  90                                  95  
 Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met  
                                   100                                  105                                  110  
 Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr  
                                   115                                  120                                  125  
 Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly  
                                   130                                  135                                  140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val  
 145 150 155 160  
 Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn  
 165 170 175  
 Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr  
 180 185 190  
 Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn  
 195 200 205  
 Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala  
 210 215 220  
 Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser  
 225 230 235 240  
 Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr  
 245 250 255  
 Lys Ile Thr Ser Ser Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val  
 260 265 270  
 Gly Ala Gly Pro Phe Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr  
 275 280 285  
 Leu Gln Thr Val Gly Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg  
 290 295 300  
 Arg Cys Gly Trp Tyr Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val  
 305 310 315 320  
 Asn Gly Phe Thr Asp Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly  
 325 330 335  
 Ile Gly Glu Ile Pro Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg  
 340 345 350  
 His Asp Glu Met Pro Leu Thr Gln Ser Glu Phe His His Ala Thr Pro  
 355 360 365  
 Ile Phe Glu Thr Met Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys  
 370 375 380  
 Thr Phe Glu Asp Leu Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu  
 385 390 395 400  
 Glu Glu Leu Ser Gly Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly  
 405 410 415  
 Arg Asp Gln Thr Ile Val Leu His Asp Val Leu Ala Asp Asn  
 420 425 430

&lt;210&gt; 961

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXA00619

&lt;400&gt; 961

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cgactagggtt agtttcgggtt cgtgggggaat aataatttgc gtg gct gat aaa aag 115
                                         Val Ala Asp Lys Lys
                                         1           5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
              10              15              20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
              25              30              35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
              40              45              50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
              55              60              65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
              70              75              80              85

atc gaa gaa ttc aat gca ctg gct' ggc cat gag cac atc cac aag ggc 403
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
              90              95              100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
              105              110              115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
              120              125              130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
              135              140              145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
              150              155              160              165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
              170              175              180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
              185              190              195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

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Gln	Asp	Met	Leu	Asp	Leu	Met	Glu	Gly	Asp	Glu	Ala	Arg	Leu	Ser	Asp		
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ctg	gaa	acc	cgc	atc	gca	gca	cac	ctc	ggc	ttt	gat	cgc	gtc	ttc	gac	787	
Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp		
	215					220				225							
tcc	gtc	ggc	cag	gtc	tac	cca	cgt	tcc	ctt	gac	ttc	gat	gca	gta	tct	835	
Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser		
	230				235					240					245		
gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883	
Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile		
				250				255						260			
cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggc	ttt	aag	gaa	ggc	931	
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly		
			265					270					275				
cag	gtc	ggc	tcc	tct	gca	atg	cct	cac	aag	atg	aac	gct	cgc	tcc	tgt	979	
Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys		
		280					285					290					
gag	cgc	gtg	ggc	ggc	ctg	cag	gtt	att	ctt	cgc	gga	tac	ctc	acc	atg		
	1027																
Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg	Gly	Tyr	Leu	Thr	Met		
	295					300					305						
gtt	gct	gat	ctt	tcc	ggc	cag	cag	tgg	aac	gaa	ggc	gat	gtc	ttc	tgc		
	1075																
Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys		
	310				315					320					325		
tcc	gtg	atc	cgc	cgc	gtt	gca	ctg	cca	gac	gca	ttc	ttc	gcg	att	gac		
	1123																
Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp		
				330					335					340			
gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggc	gca	ttc		
	1171																
Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp	Glu	Phe	Gly	Ala	Phe		
			345					350					355				
cct	gcc	atg	atc	gag	cgc	gaa	ctt	gag	cgt	tac	ctg	cca	ttc	ctg	gca		
	1219																
Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala		
		360					365					370					
act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa		
	1267																
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu		
		375				380					385						
acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gcg	gtt	gcc	ctc	aac		
	1315																
Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn		
	390				395				400					405			
atg	cgc	gaa	aat	ggc	ggc	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct		
	1363																
Met	Arg	Glu	Asn	Gly	Gly	Asp	Gln	Asp	Leu	Ile	Gln	Arg	Leu	Ala	Ala		

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410                               415                               420
gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct
1411
Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
425                               430                               435

gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg
1459
Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
440                               445                               450

ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac
1507
Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
455                               460                               465

tac cga cca ggt gag att ctt taaaggtttt taacggcgtt cac
1551
Tyr Arg Pro Gly Glu Ile Leu
470                               475

<210> 962
<211> 476
<212> PRT
<213> Corynebacterium glutamicum

<400> 962
Val Ala Asp Lys Lys Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala
1 5 10 15
Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met
20 25 30
Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
35 40 45
Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
50 55 60
Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
65 70 75 80
Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
85 90 95
His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
100 105 110
Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
115 120 125
Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
130 135 140
Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
145 150 155 160
Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
165 170 175

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Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
 210 215 220  
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
 245 250 255  
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
 260 265 270  
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met  
 275 280 285  
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg  
 290 295 300  
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu  
 305 310 315 320  
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala  
 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
 340 345 350  
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
 355 360 365  
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala  
 370 375 380  
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val  
 385 390 395 400  
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile  
 405 410 415  
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu  
 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
 435 440 445  
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His  
 450 455 460  
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu  
 465 470 475

&lt;210&gt; 963

&lt;211&gt; 666



&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(643)

&lt;223&gt; RXA00688

&lt;400&gt; 963

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gcggaaccgc aatcttgatt cttgtatctg ttgcaactgac cacagtgaag cagattgaga 60

gccagctcct gcaaagcaac tacgaaggac ttctaaaata atg cga ctc gta ctc 115
                                         Met Arg Leu Val Leu
                                         1 5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
                        10 15 20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
                        25 30 35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
                        40 45 50

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
                        55 60 65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
                        70 75 80 85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
                        90 95 100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
                        105 110 115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
                        120 125 130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
                        135 140 145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
                        150 155 160 165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
                        170 175 180

taagatttct tctctagtgc tgc 666

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<210> 964  
 <211> 181  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 964  
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     1                    5                    10                    15  
 Ala Ala Ile Leu Ser Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly  
           20                    25                    30  
 Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu  
           35                    40                    45  
 Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr  
           50                    55                    60  
 Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly  
       65                    70                    75                    80  
 Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu  
                     85                    90                    95  
 Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn  
           100                    105                    110  
 Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly  
       115                    120                    125  
 Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr  
       130                    135                    140  
 Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile  
       145                    150                    155                    160  
 Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu  
           165                    170                    175  
 Lys Ala Leu Gly Lys  
           180

<210> 965  
 <211> 531  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(508)  
 <223> RXA00266

<400> 965  
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 agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115  
   Met Thr Glu Arg Thr  
   1                    5

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ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
      10              15              20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
      25              30              35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
      40              45              50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
      55              60              65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
      70              75              80              85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
      90              95              100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
      105              110              115

ggg tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
      120              125              130

cct aac ctg taatttttac ggtagaaaa aaa 531
Pro Asn Leu
      135

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&lt;210&gt; 966

&lt;211&gt; 136

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 966

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Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn
 1              5              10              15

Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys
      20              25              30

Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys
      35              40              45

His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu
      50              55              60

Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg
      65              70              75              80

Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala
      85              90              95

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Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly  
                   100                  105                  110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu  
                   115                  120                  125

Ile Ser Ile Trp Phe Pro Asn Leu  
                   130                  135

<210> 967

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00489

<400> 967

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gtcttcgctg tatacgacca tttaagggag gcccgtcaca atg cgt gac cac gtt 115
                                         Met Arg Asp His Val
                                         1 5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163
Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp
          10          15          20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211
Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp
          25          30          35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259
Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn
          40          45          50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307
His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly
          55          60          65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355
Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg
          70          75          80          85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403
His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu
          90          95          100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451
Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala
          105          110          115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499
Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg
          120          125          130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547
Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg

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135	140	145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc			595
Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile			
150	155	160	165
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc			643
Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala			
	170	175	180
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct			691
Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala			
	185	190	195
ggt ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt			739
Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly			
	200	205	210
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca			787
Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala			
	215	220	225
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg			835
Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala			
	230	235	240
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc			883
Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile			
	250	255	260
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att			931
Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile			
	265	270	275
gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct			979
Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala			
	280	285	290
gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac			
1027			
Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His			
	295	300	305
cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag			
1075			
Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu			
	310	315	320
gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg			
1123			
Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro			
	330	335	340
tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag			
1171			
Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys			
	345	350	355
tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt			
1219			
Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			

360                                      365                                      370  
 aac taggtgtgtg tactgcctc ttc  
 1245  
 Asn  
  
 <210> 968  
 <211> 374  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 968  
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   1                                      5                                      10                                      15  
 Tyr Ser Leu Asp Asp Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser  
                                     20                                      25                                      30  
 Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp  
                                     35                                      40                                      45  
 Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe  
   50                                      55                                      60  
 Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu  
   65                                      70                                      75                                      80  
 Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val  
                                     85                                      90                                      95  
 Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu  
                                     100                                      105                                      110  
 Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg  
   115                                      120                                      125  
 Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser  
   130                                      135                                      140  
 Pro Gln Asn Val Arg Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala  
   145                                      150                                      155                                      160  
 Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn  
                                     165                                      170                                      175  
 Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp  
                                     180                                      185                                      190  
 Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His  
   195                                      200                                      205  
 Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn  
   210                                      215                                      220  
 Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile  
   225                                      230                                      235                                      240  
 Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly  
                                     245                                      250                                      255

[illegible]

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<210> 969
<211> 1545
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1531)  
<223> RXN02281
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cctataaaaag cacagtttttg aatccacagg gcatcagggc						gtg	cag	aaa	gat	agt	115							
						Val	Gln	Lys	Asp	Ser								
						1					5							
gtg	gtg	cgc	atg	gaa	gca	aca	acg	atc	gat	gac	gca	atc	gcg	aag	ctc	163		
Val	Val	Arg	Met	Glu	Ala	Thr	Thr	Ile	Asp	Asp	Ala	Ile	Ala	Lys	Leu			
				10					15					20				
att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac																211		
Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn																		
				25					30					35				
aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc																259		
Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr																		
				40					45					50				
gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc																307		
Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly																		
				55					60					65				
tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc																355		
Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg																		

70	75	80	85	
gtg att gag cgt tac	ctc cgc gaa caa ctc	gag cgt ctc acc agt aat	403	
Val Ile Glu Arg Tyr	Leu Arg Glu Gln Leu	Glu Arg Leu Thr Ser Asn		
	90	95	100	
tat ccc tgc aag att	tac gta tct gag tca	gat atc cgc atc cca ccg	451	
Tyr Pro Cys Lys Ile	Tyr Val Ser Glu Ser	Asp Ile Arg Ile Pro Pro		
	105	110	115	
gag tac att cgc ggc	gca cct tcc gct acc	gaa gct cgc cgt gct ggt	499	
Glu Tyr Ile Arg Gly	Ala Pro Ser Ala Thr	Glu Ala Arg Arg Ala Gly		
	120	125	130	
gat gtt gca gat atc	atc cca cgc ccc acc	ctg gat gaa gtc cac gac	547	
Asp Val Ala Asp Ile	Ile Pro Arg Pro Thr	Leu Asp Glu Val His Asp		
	135	140	145	
gca att atc gac ggc	gac tgg cac gcc ttc	aac ggc ccc gaa ctc ccg	595	
Ala Ile Ile Asp Gly	Asp Trp His Ala Phe	Asn Gly Pro Glu Leu Pro		
	150	155	160	165
ctt ttc cac ttc ggg	ccg caa cgc ttc gac	atc gcc tgc gcc cgc atc	643	
Leu Phe His Phe Gly	Pro Gln Arg Phe Asp	Ile Ala Cys Ala Arg Ile		
	170	175	180	
gag cac tac acc ggc	atc aac gtg gaa cac	gtg cag aag tac att ctg	691	
Glu His Tyr Thr Gly	Ile Asn Val Glu His	Val Gln Lys Tyr Ile Leu		
	185	190	195	
ttc acc aac tac gcc	atg cac acc acc gag	ttc gtg cat ttt gcc atg	739	
Phe Thr Asn Tyr Ala	Met His Thr Thr Glu	Phe Val His Phe Ala Met		
	200	205	210	
tcc gaa ctc acc tcg	gaa gac tcc cgc tac	gtg ggt cta tcc ttg cca	787	
Ser Glu Leu Thr Ser	Glu Asp Ser Arg Tyr	Val Gly Leu Ser Leu Pro		
	215	220	225	
aac ggg cag gta att	gac cga gag acc gcc	acc agc ctc ggt acg gaa	835	
Asn Gly Gln Val Ile	Asp Arg Glu Thr Ala	Thr Ser Leu Gly Thr Glu		
	230	235	240	245
acc ctt gat ctg act	agc cgt ttc caa atg	cct cgt tac gat ctc atc	883	
Thr Leu Asp Leu Thr	Ser Arg Phe Gln Met	Pro Arg Tyr Asp Leu Ile		
	250	255	260	
acc gaa gcc ggt gac	ggt att acc att atc	aac atc ggt gtg ggc cca	931	
Thr Glu Ala Gly Asp	Gly Ile Thr Ile Ile	Asn Ile Gly Val Gly Pro		
	265	270	275	
tcc aat gca aaa act	atc acc gac tgc ctt	gct gtg ctc cgc cca gaa	979	
Ser Asn Ala Lys Thr	Ile Thr Asp Cys Leu	Ala Val Leu Arg Pro Glu		
	280	285	290	
gcc tgg gtg atg atc	ggc cac tgt gct ggc	atg gac gcc cgc atg cgc		
1027				
Ala Trp Val Met Ile	Gly His Cys Ala Gly	Met Asp Ala Arg Met Arg		
	295	300	305	
atc ggc gac ctc atc	ctt ggc aac gcc tac	cag cgc gaa gac cac att		
1075				



Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
 310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
 1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
 1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
 345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
 1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
 360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc  
 1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
 375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
 1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
 390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
 1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
 410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
 1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
 425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
 1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
 440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
 1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
 455 460 465

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Thr Leu Gly Glu Val Pro Phe Arg  
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<210> 970

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val	35	40	45
Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg	50	55	60
Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr	65	70	75
Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu	85	90	95
Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp	100	105	110
Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu	115	120	125
Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu	130	135	140
Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn	145	150	155
Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile	165	170	175
Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val	180	185	190
Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe	195	200	205
Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val	210	215	220
Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr	225	230	235
Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro	245	250	255
Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn	260	265	270
Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala	275	280	285
Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met	290	295	300
Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln	305	310	315
Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile	325	330	335

Pro	Ala	Ile	Pro	Glu	Ile	Gln	Lys	Ala	Leu	Glu	Ala	Ser	Val	Asp	Glu	
			340						345			350				
Ile	Tyr	Gly	Ser	Asp	Asn	Ser	Leu	Met	Arg	Thr	Gly	Thr	Val	Leu	Ser	
			355						360			365				
Thr	Asp	Asp	Arg	Asn	Trp	Glu	Trp	His	Thr	Pro	Glu	Asn	Leu	Trp	Asn	
			370						375			380				
Trp	Leu	Lys	Gly	Ser	Thr	Ala	Ala	Ala	Val	Asp	Met	Glu	Ser	Ser	Thr	
385						390						395			400	
Leu	Ala	Thr	Asn	Gly	Tyr	Arg	Phe	Arg	Ile	Pro	Tyr	Gly	Thr	Leu	Leu	
			405						410						415	
Ser	Val	Ser	Asp	Leu	Pro	Leu	His	Ala	Val	Pro	Lys	Leu	Ser	Ala	Gln	
			420						425			430				
Ala	Gln	Ala	Phe	Tyr	Phe	Asn	Ser	Lys	Glu	Ala	His	Val	Met	Cys	Ala	
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Val	Arg	Ala	Met	Glu	Tyr	Leu	Ala	Val	Asp	Pro	Glu	Arg	Leu	Arg	Thr	
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1168)
<223> FRXA02281
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																Val	Gln	Lys	Asp	Ser	
																1				5	
gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc																163					
Val	Val	Arg	Met	Glu	Ala	Thr	Thr	Ile	Asp	Asp	Ala	Ile	Ala	Lys	Leu						
				10					15					20							
att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac																211					
Ile	Asp	Ile	Tyr	Asp	Thr	Ser	Thr	Lys	Leu	Ala	Lys	Glu	Thr	Leu	Asn						
				25					30					35							
aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc																259					
Asn	Glu	Asp	Tyr	Ala	Ala	Tyr	Ala	Asp	Val	Val	Tyr	Pro	Lys	Leu	Thr						
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gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc																307					
Val	Asp	Val	Leu	Glu	Trp	Lys	Pro	Ile	Asp	Arg	Thr	Glu	Pro	Phe	Gly						
				55					60					65							

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc	355
Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg	
70 75 80 85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	
90 95 100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg	451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	
105 110 115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
280 285 290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	
1027	
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	

atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att  
1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc  
1168

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser  
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<211> 356

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 972

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35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
 195 200 205  
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
 210 215 220  
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
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 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser  
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<210> 973  
 <211> 1302  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1279)  
 <223> RXA00147

<400> 973  
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 Val Ser Lys Asp Thr  
 1 5  
 acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163  
 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu  
 10 15 20  
 gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211  
 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile  
 25 30 35  
 ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259

Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
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Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883
Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu	
250 255 260	
gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag	931
Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln	
265 270 275	
att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc	979
Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly	

280 285 290  
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 1027  
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
 295 300 305  
 gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc  
 1075  
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly  
 310 315 320 325  
 cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc  
 1123  
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
 330 335 340  
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 1171  
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala  
 345 350 355  
 tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca  
 1219  
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
 360 365 370  
 agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag  
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 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln  
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 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95



Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
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 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
 290 295 300  
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
 355 360 365  
 Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
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 Asp Ala Asp Ala Gln Lys Lys Gly Ala  
 385 390

&lt;210&gt; 975

&lt;211&gt; 1059

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1036)

&lt;223&gt; RXA00145

&lt;400&gt; 975

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                                         Met Lys His Leu Leu
                                         1 5

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Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
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gcg gat cgc ttt aag gag gtg ctc gaa gga cgt gaa gta aag aag ctg 211
Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
              25              30              35

ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
              40              45              50

acg cgc acc cgt tcg tcc ttt gaa acc gca gga aag tgg atg agc gcc 307
Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
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Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser Val Lys Lys Gly Glu
              70              75              80              85

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Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
              90              95              100

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Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala Gln Gln Leu Ala Gln
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ttc gtc gca cca ggt ggc aac ggc ccc agc gtg atc aac gcg ggt gac 499
Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
              120              125              130

ggt tcg cac cag cac ccc acc cag gcg ctt ctc gac gct tta acc atc 547
Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
              135              140              145

cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
              150              155              160              165

gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
Asp Cys Leu His Ser Arg Val Val Arg Ser Asn Val Asp Leu Leu Ser
              170              175              180

act ttg ggc gca gag gta gtg ctg gtt gct cct ccg aca ctg ctt cct 691
Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro

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200	205 210		
gaa att gcc gac gcc gac gta gtg atg atg ctg cgc gtt cag caa gaa	787		
Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu			
215	220 225		
cgc atg cag ggt ggt ttc ttc ccc tca cac cgt gag tac gca acg ctg	835		
Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu			
230	235 240 245		
tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc	883		
Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile			
250	255 260		
atc atg cac ccc ggc ccc atg ctt cgt ggc atg gaa att aac ttc cag	931		
Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln			
265	270 275		
gtg gca gac gca cca cgc acc gcg gta ctg cag cag gta agc aac ggt	979		
Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly			
280	285 290		
gtg cac atg cgc atg gcc att ttg ttc gcc ctg gtc gca ggc tct gac			
1027			
Val His Met Arg Met Ala Ile Leu Phe Ala Leu Val Ala Gly Ser Asp			
295	300 305		
gcg act atc taatcgcgac catctgatcg cga			
1059			
Ala Thr Ile			
310			
<210> 976			
<211> 312			
<212> PRT			
<213> <i>Corynebacterium glutamicum</i>			
<400> 976			
Met Lys His Leu Leu Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val			
1	5 10 15		
Gly Leu Leu Asp Glu Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg			
20	25 30		
Glu Val Lys Lys Leu Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu			
35	40 45		
Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly			
50	55 60		
Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser			
65	70 75 80		
Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala			
85	90 95		

Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala  
 100 105 110  
 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val  
 115 120 125  
 Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu  
 130 135 140  
 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys  
 145 150 155 160  
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn  
 165 170 175  
 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro  
 180 185 190  
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser  
 195 200 205  
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu  
 210 215 220  
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg  
 225 230 235 240  
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu  
 245 250 255  
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met  
 260 265 270  
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln  
 275 280 285  
 Gln Val Ser Asn Gly Val His Met Arg Met Ala Ile Leu Phe Ala Leu  
 290 295 300  
 Val Ala Gly Ser Asp Ala Thr Ile  
 305 310

&lt;210&gt; 977

&lt;211&gt; 1464

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1441)

&lt;223&gt; RXA00146

&lt;400&gt; 977

atggccattt tgttcgccct ggtcgcaggc tctgacgcga ctatctaate gcgaccatct 60

gatcgcgaaa ttctagaaaa ggtaacgagg gattaaagaa gtg gtt gac agc aac 115  
 Val Val Asp Ser Asn  
 1 5

acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163

Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro	Ala	Pro	Ala	Asp	Ser		
				10					15					20			
ctc	cta	atc	agc	aac	gtt	ttg	gtc	tac	ggc	gaa	ggc	gag	cca	acg	aat	211	
Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn		
			25					30					35				
gtg	ttt	gtt	aaa	gat	ggc	gtg	atc	gca	gct	atc	ggc	ggc	act	cat	gag	259	
Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu		
			40				45					50					
gct	gac	cgc	acc	atc	gac	ggc	aat	ggg	gga	gtt	ctc	ctt	cca	ggc	ttc	307	
Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe		
	55					60					65						
gtg	gac	atg	cac	gtt	cac	ctg	cgt	gag	cca	ggc	cgc	gaa	gac	act	gaa	355	
Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu		
	70				75					80					85		
acc	att	gcc	act	ggc	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403	
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala		
				90				95						100			
gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451	
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile		
			105					110					115				
gcg	gaa	tcc	gta	tgg	ttc	aag	ggc	caa	aac	att	ggc	ctg	tgc	gac	gtg	499	
Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val		
		120					125					130					
cat	cca	gtt	gga	tcc	atc	acc	aag	ggc	ctt	gag	ggc	aag	gag	ctt	act	547	
His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr		
	135					140					145						
gag	ttc	ggc	atg	atg	gct	cgc	tct	gaa	gcc	aag	gtg	cgc	atg	ttc	tct	595	
Glu	Phe	Gly	Met	Met		Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe		
	150					155				160					165		
gat	gat	ggc	aag	tgc	gtc	gat	gat	cct	cag	gtc	atg	cgc	cgc	gcg	ctg	643	
Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu		
				170					175					180			
gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691	
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp		
			185					190					195				
cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggc	gaa	aac	gca	gct	739	
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala		
		200					205					210					
cgt	ctg	ggc	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787	
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val		
	215					220					225						
gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835	
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile		
	230				235				240						245		
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883	
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys		

250										255										260										
tcc cag ggc att cca atc acc gcg gaa gtc acc ccg cac cac ctc acc	931																													
Ser Gln Gly Ile Pro Ile Thr Ala Glu Val Thr Pro His His Leu Thr																														
265 270 275																														
ttg acc gat gag cgc ctg gaa acc tac gac gcg gtc aac aaa gtc aat	979																													
Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala Val Asn Lys Val Asn																														
280 285 290																														
ccg cca ctg cgc gaa agc cgc gat gcc gaa gcg ctc aag aag gcg ctt																														
1027																														
Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala Leu Lys Lys Ala Leu																														
295 300 305																														
ctc gac ggc acc atc gat gtt gtt gca acc gac cac gct cct cac ggt																														
1075																														
Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp His Ala Pro His Gly																														
310 315 320 325																														
tcc gaa gat aag tgc tgt gaa ttc gaa aac gcc aag cca ggc atg ctc																														
1123																														
Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala Lys Pro Gly Met Leu																														
330 335 340																														
gga ttg gaa acc tca ctg tcc atc atc gtg gac acc ttc gtt gcc acc																														
1171																														
Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp Thr Phe Val Ala Thr																														
345 350 355																														
gga ctt gca gac tgg cgc ttt gtt gcg cgc gtg atg agt gaa cgc cca																														
1219																														
Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val Met Ser Glu Arg Pro																														
360 365 370																														
gca gaa atc acc cgt cta cca ggc cag ggt cgc cca atc gca gaa ggt																														
1267																														
Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg Pro Ile Ala Glu Gly																														
375 380 385																														
gag cca gca aac ctc gcg att gtt gat cca gga aaa acc tgg aca gca																														
1315																														
Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly Lys Thr Trp Thr Ala																														
390 395 400 405																														
tcc ggt gca gac ttt gcg tcc aag gct gaa aat acc cca ttt gag ggc																														
1363																														
Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn Thr Pro Phe Glu Gly																														
410 415 420																														
caa gaa ttc agt gcc aag gtc aca cac acc gtg ctt cgt ggc aag gtg																														
1411																														
Gln Glu Phe Ser Ala Lys Val Thr His Thr Val Leu Arg Gly Lys Val																														
425 430 435																														
act tgt gca gac gga gtt gca caa aac gct taacgggtgg gtgcatagta																														
1461																														
Thr Cys Ala Asp Gly Val Ala Gln Asn Ala																														
440 445																														

tgc  
1464

<210> 978

<211> 447

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 978

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Val Val Asp Ser Asn Thr Gln Tyr Pro Glu Thr Gly Ala Leu Ala Pro
 1              5              10              15

Ala Pro Ala Asp Ser Leu Leu Ile Ser Asn Val Leu Val Tyr Gly Glu
      20              25              30

Gly Glu Pro Thr Asn Val Phe Val Lys Asp Gly Val Ile Ala Ala Ile
      35              40              45

Gly Gly Thr His Glu Ala Asp Arg Thr Ile Asp Gly Asn Gly Gly Val
      50              55              60

Leu Leu Pro Gly Phe Val Asp Met His Val His Leu Arg Glu Pro Gly
      65              70              75              80

Arg Glu Asp Thr Glu Thr Ile Ala Thr Gly Ser Ala Ala Ala Lys
      85              90              95

Gly Gly Phe Thr Ala Val Phe Thr Met Ala Asn Thr Thr Pro Val Met
      100              105              110

Asp Gln Pro Val Ile Ala Glu Ser Val Trp Phe Lys Gly Gln Asn Ile
      115              120              125

Gly Leu Cys Asp Val His Pro Val Gly Ser Ile Thr Lys Gly Leu Glu
      130              135              140

Gly Lys Glu Leu Thr Glu Phe Gly Met Met Ala Arg Ser Glu Ala Lys
      145              150              155              160

Val Arg Met Phe Ser Asp Asp Gly Lys Cys Val Asp Asp Pro Gln Val
      165              170              175

Met Arg Arg Ala Leu Glu Tyr Ala Lys Gly Met Asp Val Leu Ile Ala
      180              185              190

Gln His Ala Glu Asp His Arg Leu Thr Glu Gly Ala Ser Ala His Glu
      195              200              205

Gly Glu Asn Ala Ala Arg Leu Gly Leu Arg Gly Trp Pro Arg Val Ala
      210              215              220

Glu Glu Ser Ile Val Val Arg Asp Ala Ile Met Ala Arg Asp Tyr Gly
      225              230              235              240

Asn Arg Val His Ile Cys His Ala Ser Thr Glu Gly Thr Val Glu Leu
      245              250              255

Leu Arg Trp Ala Lys Ser Gln Gly Ile Pro Ile Thr Ala Glu Val Thr
      260              265              270

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Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala  
           275                          280                          285

Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala  
           290                          295                          300

Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp  
   305                          310                          315                          320

His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala  
                           325                          330                          335

Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp  
           340                          345                          350

Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val  
           355                          360                          365

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg  
           370                          375                          380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly  
   385                          390                          395                          400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn  
                           405                          410                          415

Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val  
           420                          425                          430

Leu Arg Gly Lys Val Thr Cys Ala Asp Gly Val Ala Gln Asn Ala  
           435                          440                          445

&lt;210&gt; 979

&lt;211&gt; 1025

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1002)

&lt;223&gt; RXA02208

&lt;400&gt; 979

ctc gga gtc gtc gac ggc gtc gca cct cta aac cgc acc atg gaa aaa	48
Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys	
1                          5                          10                          15	
atc atc gca gtg cac gat gat tcc ctc tcc cag gaa gtc ttc ggc gtc	96
Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val	
20                          25                          30	
acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca	144
Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala	
35                          40                          45	
tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt	192
Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu	
50                          55                          60	



ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt	240
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	
65 70 75 80	
ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac	288
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	
85 90 95	
aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc	336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	
100 105 110	
acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct	384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	
115 120 125	
gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat	432
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	
130 135 140	
ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt	480
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	
145 150 155 160	
ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca	528
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	
165 170 175	
gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac	576
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	
180 185 190	
ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc	624
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	
195 200 205	
aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc	672
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	
210 215 220	
ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc	720
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	
225 230 235 240	
tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc	768
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	
245 250 255	
tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc	816
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	
260 265 270	
agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt	864
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	
275 280 285	
ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga	912
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	
290 295 300	
gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc	960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg  
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac  
 1002

Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn  
 325 330

taaacagacc aaacacacgt gcc  
 1025

<210> 980

<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 980

Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys  
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Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val  
 20 25 30

Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala  
 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu  
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu  
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn  
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser  
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala  
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp  
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly  
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala  
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp  
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu  
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly  
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

225                      230                      235                      240  
 Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu  
                                  245                      250                      255  
 Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile  
                                  260                      265                      270  
 Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu  
                                  275                      280                      285  
 Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg  
                                  290                      295                      300  
 Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg  
 305                                   310                      315                      320  
 Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn  
                                  325                      330

<210> 981  
 <211> 675  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(652)  
 <223> RXA01660

<400> 981  
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 taaacctcaa tcatcaaatt agggaagggc tgggaaatcc atg tca tct aat tcc 115  
    Met Ser Ser Asn Ser  
    1                      5  
  
 att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163  
 Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu  
    10                      15                      20  
  
 gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat 211  
 Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp  
                                  25                      30                      35  
  
 tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259  
 Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg  
                                  40                      45                      50  
  
 ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307  
 Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp  
                                  55                      60                      65  
  
 gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355  
 Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile  
                                  70                      75                      80                      85  
  
 atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403  
 Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu  
                                  90                      95                      100

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gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg   451
Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr
      105                      110                      115

ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc   499
Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser
      120                      125                      130

cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg   547
Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val
      135                      140                      145

ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc   595
Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile
      150                      155                      160                      165

gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt   643
Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu
      170                      175                      180

gga ctc aac taacaccccc ggccccacgg agt                               675
Gly Leu Asn

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<210> 982  
 <211> 184  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 982
Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu
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Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser
      20           25           30

Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His
      35           40           45

Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala
      50           55           60

Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro
      65           70           75           80

Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe
      85           90           95

Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu
      100          105          110

Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr
      115          120          125

Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala
      130          135          140

Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly
      145          150          155          160

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Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu  
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn  
 180

<210> 983

<211> 957

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

gtgtcaccgc agctgtccag ggcataagagg ccctgcgtga gggcgttgtc agcgtccgcg 60

cgctgcagga actcgaccac gcagtcaagg cctaagccct atg aca ttc ggc gag 115  
 Met Thr Phe Gly Glu  
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163  
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile  
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211  
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val  
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259  
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp  
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307  
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly  
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355  
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu  
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403  
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser  
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451  
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu  
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499  
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu  
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547  
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val  
 135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595  
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln  
 150 155 160 165  
 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643  
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala  
 170 175 180  
 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691  
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly  
 185 190 195  
 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739  
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu  
 200 205 210  
 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787  
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala  
 215 220 225  
 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835  
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro  
 230 235 240 245  
 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883  
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met  
 250 255 260  
 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931  
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg  
 265 270 275  
 tca tagtcgcgga aacggccctt aat 957  
 Ser

&lt;210&gt; 984

&lt;211&gt; 278

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 984

Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg  
 1 5 10 15  
 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly  
 20 25 30  
 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val  
 35 40 45  
 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe  
 50 55 60  
 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile  
 65 70 75 80  
 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg  
 85 90 95

gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211  
Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp  
25 30 35

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aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att 259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile
      40                      45                      50

gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag 307
Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln
      55                      60                      65

cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc 355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly
      70                      75                      80                      85

aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc 403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly
      90                      95                      100

gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa 451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu
      105                      110                      115

cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt 499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val
      120                      125                      130

gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc 547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr
      135                      140                      145

act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg 595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met
      150                      155                      160                      165

gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca 643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro
      170                      175                      180

gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag 691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys
      185                      190                      195

ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac 739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn
      200                      205                      210

aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct 787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala
      215                      220                      225

cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
      230                      235                      240

tgatacatattt agtcttataa aca 852

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&lt;210&gt; 986

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 986

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15  
 Leu Lys Leu Gly Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30  
 Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45  
 Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60  
 Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80  
 Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95  
 Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110  
 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125  
 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140  
 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160  
 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175  
 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190  
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205  
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220  
 Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240  
 Val Glu Ser

&lt;210&gt; 987

&lt;211&gt; 798

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (47) .. (775)

&lt;223&gt; FRXA01892

&lt;400&gt; 987

atgttataaaag cggttggcac aaccctact gaaggagaac accacggtg acc acc tcg 58															
Val Thr Thr Ser 1															
agt gaa caa ccc cgt aca gga tac aaa cga gtg atg tta aag ctc gaa 106	Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu 20	5 10 15 20													
ggt gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154	Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val 35	25 30 35													
gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202	Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu 50	40 45 50													
att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250	Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu 65	55 60 65													
cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298	Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu 80	70 75 80													
ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346	Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His 100	85 90 95 100													
ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394	Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala 115	105 110 115													
gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442	Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg 130	120 125 130													
gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490	Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp 145	135 140 145													
acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538	Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu 160	150 155 160													
atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586	Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn 180	165 170 175 180													
cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634	Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu 195	185 190 195													
aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682	Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp 210	200 205 210													
aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730	Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile 225	215 220 225													
gct cgc gcc atc agc ggt gaa cgt atc qgt act ctg gtc gag tcc 775															

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser  
 230 235 240

tgatacattt agtcttataa aca

798

<210> 988

<211> 243

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15

Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30

Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240

Val Glu Ser

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<210> 989
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA00105

<400> 989
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cgaggagaat ggaacttact aacgctgtta tgatgacggc atg act gtt cca acg 115
Met Thr Val Pro Thr
1 5
cct tat gaa gac ctt ctt cgg aag att gct gaa gaa ggg tcc cac aag 163
Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu Glu Gly Ser His Lys
10 15 20
gac gac cgc acc ggc acc ggc act act tct tta ttc gga caa caa atc 211
Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu Phe Gly Gln Gln Ile
25 30 35
cgc ttt gat ctc aat gaa ggt ttt ccc ctt ctg acc acc aag aag gtc 259
Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu Thr Thr Lys Lys Val
40 45 50
cat ttc cac tct gtt gtg ggt gag ctt ttg tgg ttc ctt cag ggg gat 307
His Phe His Ser Val Val Gly Glu Leu Leu Trp Phe Leu Gln Gly Asp
55 60 65
tcc aac gtc aaa tgg ctg cag gat aac aac atc cgc att tgg aat gaa 355
Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile Arg Ile Trp Asn Glu
70 75 80 85
tgg gca gat gag gac ggc gag ctg ggc cct gtt tat ggt gtc cag tgg 403
Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val Tyr Gly Val Gln Trp
90 95 100
cgt tct tgg cca acc cct gat ggt cgt cac att gac cag atc tca ggt 451
Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile Ser Gly
105 110 115
gct tta gaa act ctg cga aac aac cct gat tca cgt cgc aat att gtc 499
Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser Arg Arg Asn Ile Val
120 125 130
tcg gcg tgg aat gtt tcc gag ctt gaa aac atg gct ctt ccc cct tgt 547
Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met Ala Leu Pro Pro Cys
135 140 145
cac ttg ctt ttc cag ctc tat gtc gcc gat ggc aaa ctg tct tgc cag 595
His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly Lys Leu Ser Cys Gln
150 155 160 165
ctc tac cag cgt tct gcg gac atg ttc ctg ggt gtg cct ttc aac atc 643
Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly Val Pro Phe Asn Ile
170 175 180

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gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691  
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu  
                   185                                  190                                  195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739  
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp  
                   200                                  205                                  210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785  
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg  
                   215                                  220                                  225

cctacccac ctt 798

<210> 990

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 990

Met Thr Val Pro Thr Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu  
           1                                  5                                  10                                  15

Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu  
                   20                                  25                                  30

Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu  
                   35                                  40                                  45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp  
           50                                  55                                  60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile  
           65                                  70                                  75                                  80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val  
                   85                                  90                                  95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile  
                   100                                  105                                  110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser  
                   115                                  120                                  125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met  
           130                                  135                                  140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly  
           145                                  150                                  155                                  160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly  
                   165                                  170                                  175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala  
                   180                                  185                                  190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp  
                   195                                  200                                  205

Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210 215 220

Arg  
225

<210> 991  
<211> 732  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(709)  
<223> RXA00131

<400> 991  
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acgttgcagg cccattcaag ccggagcact accgctacta atg att gtc agc att 115  
Met Ile Val Ser Ile  
1 5

gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163  
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr  
10 15 20

cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211  
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser  
25 30 35

att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259  
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp  
40 45 50

ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307  
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg  
55 60 65

cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355  
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp  
70 75 80 85

cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403  
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp  
90 95 100

gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451  
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly  
105 110 115

ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499  
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val  
120 125 130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547  
Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala  
135 140 145

cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595  
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

150                      155                      160                      165  
 cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg 643  
 His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val  
                                  170                      175                      180  
  
 gtt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa 691  
 Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu  
                                  185                      190                      195  
  
 ttc ctg ggt act ata aac taatcccaat tagcaggaag gat 732  
 Phe Leu Gly Thr Ile Asn  
                                  200

&lt;210&gt; 992

&lt;211&gt; 203

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 992

Met Ile Val Ser Ile Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu  
   1                                  5                                  10                                  15  
  
 Val Ser Ala Leu Thr Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro  
                                   20                                  25                                  30  
  
 Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His  
                                   35                                  40                                  45  
  
 Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu  
                                   50                                  55                                  60  
  
 Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly  
   65                                  70                                  75                                  80  
  
 Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala  
                                   85                                  90                                  95  
  
 Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu  
                                  100                                 105                                 110  
  
 Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp  
                                  115                                 120                                 125  
  
 Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu  
                                  130                                 135                                 140  
  
 Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln  
  145                                 150                                 155                                 160  
  
 Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu  
                                  165                                 170                                 175  
  
 Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala  
                                  180                                 185                                 190  
  
 Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn  
                                  195                                 200

<210> 993  
<211> 531  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101) .. (508)  
<223> RXA00266
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[illegible]

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<210> 994
<211> 136
<212> PRT
<213> Corynebacterium glutamicum
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<400> 994  
Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn



1	5	10	15
Gly His Val	Gly Glu Ile Ile	Ala Arg Ile Glu Arg Lys	Gly Leu Lys
	20	25	30
Leu Ala Ala	Leu Asp Leu Arg	Val Ala Asp Arg Glu Thr	Ala Glu Lys
	35	40	45
His Tyr Glu	Glu His Ala Asp Lys	Pro Phe Phe Gly Glu	Leu Val Glu
	50	55	60
Phe Ile Thr	Ser Ala Pro Leu Ile	Ala Gly Ile Val Glu	Gly Glu Arg
	65	70	75
Ala Ile Asp	Ala Trp Arg Gln	Leu Ala Gly Gly Thr	Asp Pro Val Ala
	85	90	95
Lys Ala Thr	Pro Gly Thr Ile Arg	Gly Asp Phe Ala Leu	Thr Val Gly
	100	105	110
Glu Asn Val	Val His Gly Ser Asp	Ser Pro Glu Ser Ala	Glu Arg Glu
	115	120	125
Ile Ser Ile	Trp Phe Pro Asn	Leu	
	130	135	

&lt;210&gt; 995

&lt;211&gt; 831

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(808)

&lt;223&gt; RXA00718

&lt;400&gt; 995

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gcaccaagct gcacaccgtt cagcttggtg atcagaagcc aggttccctt cgtgcactga 60
actcctctga gctgaccagc ttatacaagg tgggtccaact gtg acg gaa att tcc 115
                                   Val Thr Glu Ile Ser
                                   1 5
aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
                                   10 15 20
acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
                                   25 30 35
aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259
Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
                                   40 45 50
ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
                                   55 60 65
acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355

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Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp Pro Ala Ser Thr Glu
 70                      75                      80                      85

gtg ttg ctc gcg ggc gtc gat gtg caa aag gac atc cgc gga cca gaa 403
Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp Ile Arg Gly Pro Glu
                      90                      95                      100

gtc acc caa aat gtc tcc gca gtg tcc gcg atc cct gag gtt cgt gaa 451
Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile Pro Glu Val Arg Glu
                      105                      110                      115

aac ttg gtg gcg ttg cag cgc gca ctc gcc gcc aaa gca cat cgc tgc 499
Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala Lys Ala His Arg Cys
                      120                      125                      130

gtc gtc gaa ggc aga gac atc gga acg gca gtg ctt gtc gac gcg ccc 547
Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val Leu Val Asp Ala Pro
                      135                      140                      145

atc aag gcg ttt ctc acc gcc tca gcg gaa gtc cgc gcc cag cga cgc 595
Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val Arg Ala Gln Arg Arg
150                      155                      160                      165

ttt gac caa gac acc gca gca ggt cgc gac gta gat ttc gac gct gtg 643
Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val Asp Phe Asp Ala Val
                      170                      175                      180

ctg gca gat gtt gtt cgc cgc gat gaa cta gat tcc acc cgt gcc gcc 691
Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp Ser Thr Arg Ala Ala
                      185                      190                      195

tca ccg ctg aaa cca gca gat gat gca cac atc gtg gac acc tct gat 739
Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile Val Asp Thr Ser Asp
                      200                      205                      210

atg acc atg gat caa gta ctt gat cac ctc atc cac cta gtg gaa gcc 787
Met Thr Met Asp Gln Val Leu Asp His Leu Ile His Leu Val Glu Ala
                      215                      220                      225

tcc gct gaa agg agc aac cag tgactgataa acacaccatg cct 831
Ser Ala Glu Arg Ser Asn Gln
230                      235

```

&lt;210&gt; 996

&lt;211&gt; 236

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 996

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Val Thr Glu Ile Ser Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile
 1                      5                      10                      15

Asp Gly Pro Ser Gly Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala
                20                      25                      30

Thr Arg Leu Ser Ala Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val
 35                      40                      45

Ala Thr Leu His Val Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala
 50                      55                      60

```

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp  
65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp  
85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile  
100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala  
115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val  
130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val  
145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val  
165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp  
180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile  
195 200 205

Val Asp Thr Ser Asp Met Thr Met Asp Gln Val Leu Asp His Leu Ile  
210 215 220

His Leu Val Glu Ala Ser Ala Glu Arg Ser Asn Gln  
225 230 235

&lt;210&gt; 997

&lt;211&gt; 1785

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1762)

&lt;223&gt; RXA01599

&lt;400&gt; 997

caccgaacgt ttaagttttc cgcaccgcct gactcgaaaa gatctttttt aaagagctgt 60

tcgatgttta ggttcaacca ggaaggtcgt ctcagacatc atg acc tct agt cga 115  
Met Thr Ser Ser Arg  
1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163  
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser  
10 15 20

tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211  
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile  
25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

Ala	Arg	Gly	Leu	Ser	Val	Thr	Met	Gln	Lys	Leu	Asp	Pro	Tyr	Leu	Asn	
		40					45					50				
gtt	gat	ccg	ggc	acc	atg	aat	cct	ttt	gaa	cac	ggg	gaa	gtc	ttt	gtc	307
Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
		55				60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
		70			75					80					85	
ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
				90					95					100		
gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggg	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
			105					110					115			
aaa	act	gtg	cag	gtc	atc	cca	cac	atc	act	gat	gag	atc	aaa	gct	cgt	499
Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
att	ttg	agc	atg	ggc	gaa	cca	gat	gct	cat	ggg	aac	gcc	cca	gac	gtg	547
Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
		135				140					145					
gtg	atc	tct	gag	gtc	ggg	ggc	acc	gtc	ggg	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
		150			155					160					165	
ttc	ctt	gaa	gca	gct	cgc	cag	gta	cgc	cat	gaa	att	ggg	cgt	gaa	aac	643
Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
			170						175					180		
tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggg	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190					195			
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205				210					
atc	ggg	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
		215				220					225					
cct	caa	ggg	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	gtt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
		230			235					240					245	
gaa	ggc	gtt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
			250					255						260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
			265				270						275			
ggc	ctt	ccg	ttc	cgt	gat	gtt	gac	tgg	agc	acc	tgg	cac	gat	ctg	ctg	979
Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	

280	285	290
gaa cgg gtg aac aac cca cgc cat gag ctc acc gtc ggc atc gtg ggc		
1027		
Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly		
295	300	305
aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt		
1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val		
310	315	320 325
cgc gct gca ggc tac gcc aat tgg acg cgc acc aat atc aag tgg att		
1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile		
	330	335 340
acc tca gat gat tgc gaa acc cca tct ggc gcc atg aaa gcg ctc agc		
1171		
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser		
	345	350 355
ggg ttg gat gcc atc gtg gtt ccc gga ggt ttc ggt atc cga ggt atc		
1219		
Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile		
	360	365 370
gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg		
1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro		
	375	380 385
ctt ctt ggc cta tgc ctt ggc ctg cag tgc acc gtc atc gag gca gca		
1315		
Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr Val Ile Glu Ala Ala		
390	395	400 405
cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct		
1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala		
	410	415 420
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg		
1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val		
	425	430 435
tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct		
1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro		
	440	445 450
gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg		
1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr		
	455	460 465
gaa gtc tcc gag cgc cac cgt cac cgc tat gag gtc aat aat gcc tac		
1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr		
470	475	480 485

cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca  
1603

Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser  
490 495 500

cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat  
1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His  
505 510 515

cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca  
1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro  
520 525 530

acc cat gct cat cca ctg ttt tac ggc ctg gtg aag acc gct ttg gag  
1747

Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu  
535 540 545

ctg cgt gtc cac cct tagatctaca atgtgatcat ggt  
1785

Leu Arg Val His Pro  
550

<210> 998

<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 998

Met Thr Ser Ser Arg Lys Val Arg Pro Thr Lys His Ile Phe Val Thr  
1 5 10 15

Gly Gly Val Val Ser Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu  
20 25 30

Gly Gln Leu Leu Ile Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu  
35 40 45

Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His  
50 55 60

Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu  
65 70 75 80

Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn  
85 90 95

Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg  
100 105 110

Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp  
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly  
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

145		150		155		160
Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu						
		165		170		175
Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr						
		180		185		190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val						
		195		200		205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg						
		210		215		220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met						
		225		230		235
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser						
		245		250		255
Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe						
		260		265		270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr						
		275		280		285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr						
		290		295		300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser						
		305		310		315
Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr						
		325		330		335
Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala						
		340		345		350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe						
		355		360		365
Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg						
		370		375		380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr						
		385		390		395
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr						
		405		410		415
Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu						
		420		425		430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg						
		435		440		445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu						
		450		455		460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu						
		465		470		475
						480

Val Asn Asn Ala Tyr Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val  
485 490 495

Phe Ser Gly Thr Ser Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr  
500 505 510

Pro Lys Glu Val His Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu  
515 520 525

Tyr Lys Ser Arg Pro Thr His Ala His Pro Leu Phe Tyr Gly Leu Val  
530 535 540

Lys Thr Ala Leu Glu Leu Arg Val His Pro  
545 550

&lt;210&gt; 999

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3439)

&lt;223&gt; RXN02234

&lt;400&gt; 999

acccagaggc cgctgccggc ccaaattgatg caagccccct gtttgaccag tttgttgagc 60

tgatggatgc agacgctcag aagaaaggcg cataaataac atg cca aag cgt tca 115  
Met Pro Lys Arg Ser  
1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163  
Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly  
10 15 20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211  
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu  
25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259  
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr  
40 45 50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307  
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile  
55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355  
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly  
70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403  
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu  
90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451  
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly  
105 110 115



gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499  
 Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp  
 120 125 130

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547  
 Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala  
 135 140 145

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595  
 Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala  
 150 155 160 165

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643  
 Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly  
 170 175 180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691  
 Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala  
 185 190 195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739  
 Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu  
 200 205 210

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787  
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr  
 215 220 225

gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835  
 Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu  
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883  
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu  
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931  
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile  
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979  
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile  
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg  
 1027  
 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val  
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc  
 1075  
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala  
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc  
 1123  
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr  
 330 335 340

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aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac
1171
Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp
345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc
1219
Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly
360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg
1267
Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met
375 380 385

tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc
1315
Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser
390 395 400 405

ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc
1363
Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe
410 415 420

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag
1411
Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys
425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt
1459
Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu
440 445 450

ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg
1507
Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp
455 460 465

ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt
1555
Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val
470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg
1603
Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met
490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc
1651
Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly
505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta
1699
Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val
520 525 530

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ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg  
1747

Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro  
535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc  
1795

Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val  
550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca  
1843

Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro  
570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca  
1891

Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala  
585 590 595

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Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc  
2784

Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca  
2832

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc  
2880

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc  
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat  
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt  
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg  
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val  
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct  
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg  
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc  
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala  
1060 1065

gag  
3221

<210> 1002

<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 1002

Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His  
1 5 10 15

Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala  
20 25 30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu  
35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
50 55 60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala  
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr  
85 90 95

Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu  
100 105 110

Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro  
115 120 125

Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu  
130 135 140

Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala  
145 150 155 160

Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu  
165 170 175

Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile  
180 185 190

Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val  
195 200 205

Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp  
210 215 220

Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys  
225 230 235 240

Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile  
245 250 255

Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala  
260 265 270

Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr  
 275 280 285  
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala  
 290 295 300  
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala  
 305 310 315 320  
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys  
 325 330 335  
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu  
 340 345 350  
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr  
 355 360 365  
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala  
 370 375 380  
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val  
 385 390 395 400  
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala  
 405 410 415  
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln  
 420 425 430  
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu  
 435 440 445  
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu  
 450 455 460  
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser  
 465 470 475 480  
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu  
 485 490 495  
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro  
 500 505 510  
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu  
 515 520 525  
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp  
 530 535 540  
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu  
 545 550 555 560  
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp  
 565 570 575  
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met  
 580 585 590  
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile



595	600	605
Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys		
610	615	620
Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met		
625	630	635
Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu		
	645	650
Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr		
	660	665
Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val		
	675	680
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu		
	690	695
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu		
	705	710
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu		
	725	730
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu		
	740	745
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met		
	755	760
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys		
	770	775
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala		
	785	790
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser		
	805	810
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys		
	820	825
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp		
	835	840
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp		
	850	855
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg		
	865	870
Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys		
	885	890
Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr		
	900	905
Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr		
	915	920
		925

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
 945 950 955 960

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
 965 970 975

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
 980 985 990

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
 995 1000 1005

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val  
 1010 1015 1020

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
 1025 1030 1035 1040

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
 1045 1050 1055

Leu Gln Glu Leu Asp His Ala Val Lys Ala  
 1060 1065

&lt;210&gt; 1003

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(424)

&lt;223&gt; RXN00450

&lt;400&gt; 1003

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115  
 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu  
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val  
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg  
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc gcc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
 90 95 100

ggt gct cga atc gga cgc atc 424  
 Gly Ala Arg Ile Gly Arg Ile  
 105

<210> 1004

<211> 108

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1004

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile  
 100 105

<210> 1005

<211> 418

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1005

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gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg gcc gtt tta cct 115  
 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

	10	15	20	
gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc				211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val				
	25	30	35	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga				259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
	40	45	50	
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga				307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
	70	75	80	85
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
	90	95	100	
ggt gct cga atc gga				418
Gly Ala Arg Ile Gly				
	105			

&lt;210&gt; 1006

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1006

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
100 105

&lt;210&gt; 1007

&lt;211&gt; 1368

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; RXN02272

&lt;400&gt; 1007

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tatttaactc cacactaata cctgtcaagc aatagaatag atagcatctg gatcctccag 60

agtttgaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115
                                   Val Arg Ile Thr Asn
                                   1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
                                   10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
                                   25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
                                   40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
                                   55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
                                   70 75 80 85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
                                   90 95 100

aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
                                   105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
                                   120 125 130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
                                   135 140 145

att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
                                   150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
                                   170 175 180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
                                   185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His

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200	205	210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc			787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala			
215	220	225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat			835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His			
230	235	240	245
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta			883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu			
250	255	260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa			931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu			
265	270	275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt			979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly			
280	285	290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt			
1027			
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe			
295	300	305	
tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat			
1075			
Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp			
310	315	320	325
cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca			
1123			
Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr			
330	335	340	
gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc			
1171			
Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala			
345	350	355	
gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg			
1219			
Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala			
360	365	370	
aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga			
1267			
Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg			
375	380	385	
aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc			
1315			
Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser			
390	395	400	405
agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc			
1365			
Arg Glu Pro Glu Gln Val Asp Trp Asn Ile			
410	415		

ctt  
1368

<210> 1008

<211> 415

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1008

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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile  
20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg  
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala  
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu  
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys  
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu  
100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr  
115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu  
130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala  
145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala  
165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly  
180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala  
195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe  
210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln  
225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr  
245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala  
260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
 275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
 290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
 305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
 325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
 340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
 355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
 370 375 380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
 385 390 395 400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
 405 410 415

&lt;210&gt; 1009

&lt;211&gt; 1368

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; FRXA02272

&lt;400&gt; 1009

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agtttgaaaa tatgccttga catgtagaaa tggagttcgtg cgc att aca aac 115  
 Val Arg Ile Thr Asn  
 1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163  
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly  
 10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211  
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp  
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259  
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln  
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307  
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile  
 55 60 65



cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa	499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag	595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt	979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly	
280 285 290	
ggt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt	1027
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe	
295 300 305	

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat  
 1075  
 Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp  
 310 315 320 325  
  
 cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca  
 1123  
 Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr  
 330 335 340  
  
 gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc  
 1171  
 Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala  
 345 350 355  
  
 gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg  
 1219  
 Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala  
 360 365 370  
  
 aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga  
 1267  
 Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg  
 375 380 385  
  
 aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc  
 1315  
 Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser  
 390 395 400 405  
  
 agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc  
 1365  
 Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
 410 415

ctt  
 1368

<210> 1010  
 <211> 415  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 1010  
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 1 5 10 15  
  
 Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile  
 20 25 30  
  
 Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg  
 35 40 45  
  
 Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala  
 50 55 60  
  
 Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu  
 65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys  
                                     85                                    90                                    95  
 Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu  
                                     100                                    105                                    110  
 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr  
                                     115                                    120                                    125  
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu  
                                     130                                    135                                    140  
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala  
                                     145                                    150                                    155                                    160  
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala  
                                     165                                    170                                    175  
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly  
                                     180                                    185                                    190  
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala  
                                     195                                    200                                    205  
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe  
                                     210                                    215                                    220  
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln  
                                     225                                    230                                    235                                    240  
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr  
                                     245                                    250                                    255  
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala  
                                     260                                    265                                    270  
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
                                     275                                    280                                    285  
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
                                     290                                    295                                    300  
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
                                     305                                    310                                    315                                    320  
 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
                                     325                                    330                                    335  
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
                                     340                                    345                                    350  
 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
                                     355                                    360                                    365  
 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
                                     370                                    375                                    380  
 Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
                                     385                                    390                                    395                                    400  
 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

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405                                410                                415

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(580)
<223> RXN03004

<400> 1011
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cgtggcccaa ccctgaacgc tgaacgctac actggttgac gtg ctt ctt tca gat 115
                               Val Leu Leu Ser Asp
                               1 5

cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct 163
Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro
      10 15 20

ttc gac gct gag ctg att cag ccg tcg agt gtc gat gtc cgc atg gac 211
Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp
      25 30 35

cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct 259
Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro
      40 45 50

aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc 307
Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly
      55 60 65

gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg 355
Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu
      70 75 80 85

gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403
Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys
      90 95 100

tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451
Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe
      105 110 115

att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499
Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val
      120 125 130

gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547
Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu
      135 140 145

gct ttg ttc cag atg agt tcc cct gcg gag act 580
Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
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<210> 1012  
 <211> 160  
 <212> PRT  
 <213> Corynebacterium glutamicum

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 Leu Gly Ile Glu Pro Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val  
                     20                    25                    30  
 Asp Val Arg Met Asp Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr  
             35                    40                    45  
 Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val  
             50                    55                    60  
 Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val  
     65                    70                    75                    80  
 Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly  
                     85                    90                    95  
 Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His  
             100                    105                    110  
 Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu  
             115                    120                    125  
 Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met  
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 Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr  
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<210> 1013  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(202)  
 <223> RXN03137

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 cgcgagcag ctgagccgat aagctcgccc ctacccacc ttg gag ctc aac aag 115  
   Leu Glu Leu Asn Lys  
   1                    5  
 gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163  
 Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly  
                     10                    15                    20

tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcggtgc 212  
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val  
                   25                                  30

gatttgggca caa 225

<210> 1014

<211> 34

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

Leu Glu Leu Asn Lys Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp  
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Ile Thr Val Ser Gly Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val  
                   20                                  25                                  30

Ala Val

<210> 1015

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1015

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cggctcttctt ctgggaggca atgatttaac atgtgaagct atg gac atc acc atc 115  
   Met Asp Ile Thr Ile  
   1                                  5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
                                   10                                  15                                  20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
                   25                                  30                                  35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
                   40                                  45                                  50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
                   55                                  60                                  65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
   70                                  75                                  80                                  85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
                                   90                                  95                                  100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
                                   105                                  110                                  115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
                                   120                                  125                                  130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt gcc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
                                   135                                  140                                  145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
                                   150                                  155                                  160                                  165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
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&lt;210&gt; 1016

&lt;211&gt; 171

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1016

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
                                   20                                  25                                  30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
                                   35                                  40                                  45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
                                   50                                  55                                  60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
                                   65                                  70                                  75                                  80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
                                   85                                  90                                  95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
                                   100                                  105                                  110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
                                   115                                  120                                  125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
                                   130                                  135                                  140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
                                   145                                  150                                  155                                  160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser

165

170

<210> 1017  
 <211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(613)  
 <223> FRXA02857

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 Met Asp Ile Thr Ile  
 1 5  
 gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20  
 cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35  
 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50  
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65  
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85  
 gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100  
 cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115  
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130  
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145  
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165  
 gac gca ttg gcg gaa tct 613



Asp Ala Leu Ala Glu Ser  
170

<210> 1018  
<211> 171  
<212> PRT  
<213> Corynebacterium glutamicum

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20 25 30  
Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
35 40 45  
Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
50 55 60  
Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
65 70 75 80  
Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
85 90 95  
Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
100 105 110  
Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
115 120 125  
Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
130 135 140  
Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
145 150 155 160  
Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
165 170

<210> 1019  
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atggaacatg gaccgttggt ccagaagtga ggaataagta gtg agc gaa caa gct 115  
Val Ser Glu Gln Ala  
1 5

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cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163
Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg
              10              15              20

tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211
Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr
              25              30              35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259
Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met
              40              45              50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307
Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp
              55              60              65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355
Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu
              70              75              80              85

ggg gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403
Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val
              90              95              100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451
Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro
              105              110              115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499
Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp
              120              125              130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547
Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu
              135              140              145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595
Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro
              150              155              160              165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643
Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val
              170              175              180

aga gat cct cag tagaaggatc gaaagaaagg cgg 678
Arg Asp Pro Gln
              185

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&lt;210&gt; 1020

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1020

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Val Ser Glu Gln Ala Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu
  1              5              10              15

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Asp Lys Lys Thr Arg Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu
              20              25              30

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Phe	Glu	Asp	Leu	Thr	Pro	Val	Leu	Gly	Asp	Ala	Glu	Ser	Phe	Val	Ala
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Val	Val	Asp	Ala	Met	Ala	Glu	Ala	Ala	Glu	Lys	Leu	Asn	Ala	Glu	Ile
50						55						60			
Ile	Gly	Gly	Leu	Asp	Ala	Arg	Gly	Phe	Leu	Leu	Gly	Ser	Ala	Val	Ala
65						70						75			
Tyr	Lys	Leu	Gly	Leu	Gly	Val	Leu	Ala	Ile	Arg	Lys	Lys	Gly	Lys	Leu
			85						90			95			
Pro	Pro	Pro	Val	Val	Thr	Gln	Glu	Tyr	Glu	Leu	Glu	Tyr	Gly	Thr	Ala
			100						105			110			
Ala	Leu	Glu	Leu	Pro	Ser	Glu	Gly	Ile	Asp	Ile	Ala	Gly	Lys	Asn	Ile
115						120						125			
Val	Leu	Ile	Asp	Asp	Val	Leu	Ala	Thr	Gly	Gly	Thr	Leu	Gly	Ala	Ala
130						135						140			
Arg	Lys	Leu	Ile	Glu	Ser	Cys	Asp	Gly	His	Val	Ser	Gly	Tyr	Val	Leu
145						150						155			
Ala	Ile	Glu	Val	Pro	Gly	Leu	Gly	Gly	Arg	Asp	Asn	Leu	Gly	Asp	Arg
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Pro	Val	Ile	Val	Val	Arg	Asp	Pro	Gln							
			180			185									

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(700)  
<223> RXA01512
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tgattgacac ctgaatctac aacacaaggg gaacgcgacg atg agc aac aac gta 115
Met Ser Asn Asn Val
1 5

gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163
Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly
10 15 20

acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211
Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg
25 30 35

atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259
Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu
40 45 50

gaa gac ctc atc ctg gtg tgc gtg ctc aaq qgc qcq ttc tac ttc ctg 307

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Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu  
 55 60 65  
 gca gat ttc tcc cgc atg ctc gac atc ccc acc cag tcc gag ttc atg 355  
 Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met  
 70 75 80 85  
 gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403  
 Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg  
 90 95 100  
 atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451  
 Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile  
 105 110 115  
 gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499  
 Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg  
 120 125 130  
 aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547  
 Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu  
 135 140 145  
 cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595  
 Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly  
 150 155 160 165  
 ttt gat att cca aat gag ttt gtt gtg ggc tac gga ctt gat ttc gca 643  
 Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala  
 170 175 180  
 gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691  
 Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr Leu Glu Pro His Val  
 185 190 195  
 tac tcc gac tagtaatcaa aagtgcgaaa gag 723  
 Tyr Ser Asp  
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&lt;210&gt; 1022

&lt;211&gt; 200

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1022

Met Ser Asn Asn Val Glu Met Ala Asp His Lys Asp Leu Asn Val Pro  
 1 5 10 15  
 Ala Asn Pro Tyr Gly Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu  
 20 25 30  
 Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu  
 35 40 45  
 Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly  
 50 55 60  
 Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr  
 65 70 75 80

Gln	Ser	Glu	Phe	Met	Ala	Val	Ser	Ser	Tyr	Gly	Asn	Ser	Thr	Ser	Ser
				85					90					95	
Ser	Gly	Val	Val	Arg	Ile	Leu	Lys	Asp	Leu	Asp	Lys	Glu	Ile	Glu	Gly
			100					105					110		
Arg	Asp	Val	Leu	Ile	Val	Glu	Asp	Ile	Ile	Asp	Ser	Gly	Leu	Thr	Leu
		115					120					125			
Ser	Trp	Leu	Met	Arg	Asn	Leu	Lys	Asn	Arg	Asn	Pro	Lys	Ser	Leu	Asn
	130					135					140				
Val	Ile	Thr	Leu	Leu	Arg	Lys	Pro	Glu	Arg	Leu	Thr	Thr	Asn	Ile	Asp
145					150					155					160
Met	Phe	Asp	Ile	Gly	Phe	Asp	Ile	Pro	Asn	Glu	Phe	Val	Val	Gly	Tyr
				165					170					175	
Gly	Leu	Asp	Phe	Ala	Glu	Arg	Tyr	Arg	Asp	Leu	Pro	Tyr	Val	Gly	Thr
			180					185					190		
Leu	Glu	Pro	His	Val	Tyr	Ser	Asp								
		195					200								

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<210> 1023
<211> 597
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA02031
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ttgcagaacg	ttgaagcatc	attgactagg	atatgtagac	atg	aca	gag	gaa	cgc								115
				Met	Thr	Glu	Glu	Arg								
				1				5								
gag	att	ctg	acc	tat	gag	atg	ttc	gga	aca	gca	atg	cgg	gag	ctg	gcc	163
Glu	Ile	Leu	Thr	Tyr	Glu	Met	Phe	Gly	Thr	Ala	Met	Arg	Glu	Leu	Ala	
				10					15					20		
caa	gaa	att	att	gat	gac	tac	cag	cca	gat	tgc	gtg	ctg	tcc	att	gcg	211
Gln	Glu	Ile	Ile	Asp	Asp	Tyr	Gln	Pro	Asp	Cys	Val	Leu	Ser	Ile	Ala	
				25					30					35		
cgt	ggg	ggg	ctt	cta	atc	ggg	ggc	gca	ctt	ggg	tat	gcg	ctg	ggg	atc	259
Arg	Gly	Gly	Leu	Leu	Ile	Gly	Gly	Ala	Leu	Gly	Tyr	Ala	Leu	Gly	Ile	
				40					45					50		
aag	aat	gta	tcg	gtg	atc	aat	gtg	gag	ttc	tac	acc	gat	att	gga	gag	307
Lys	Asn	Val	Ser	Val	Ile	Asn	Val	Glu	Phe	Tyr	Thr	Asp	Ile	Gly	Glu	
				55					60					65		
cac	ttg	gag	gag	cca	atg	atg	ctg	cct	cca	act	cca	aaa	gct	ggt	gat	355
His	Leu	Glu	Glu	Pro	Met	Met	Leu	Pro	Pro	Thr	Pro	Lys	Ala	Val	Asp	
70					75					80					85	

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ctc tcg gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403
Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp Val Ala Asp Thr Gly
          90                      95                      100

aag act ctt gag ttg gtc agg gac ttc ctg ggt gac caa gtt gtc gaa 451
Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu
          105                      110                      115

gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499
Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro
          120                      125                      130

gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547
Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser
          135                      140                      145

acc ctg cct cca gtg gag cct tct aag taatttttca cccgtgaaag 594
Thr Leu Pro Pro Val Glu Pro Ser Lys
150                      155

tgc 597

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<210> 1024
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

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<400> 1024
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Met Arg Glu Leu Ala Gln Glu Ile Ile Asp Asp Tyr Gln Pro Asp Cys
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Val Leu Ser Ile Ala Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly
          35                      40                      45

Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr
          50                      55                      60

Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr
          65                      70                      75                      80

Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp
          85                      90                      95

Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly
          100                      105                      110

Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn
          115                      120                      125

Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile
          130                      135                      140

Asn Phe Pro Trp Ser Thr Leu Pro Pro Val Glu Pro Ser Lys
          145                      150                      155

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<210> 1025  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(730)  
 <223> RXA00981

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 ggatagaagt acccccagtc cagaatgaag gtcaccacca atg tca gag aat ttg 115  
 Met Ser Glu Asn Leu  
 1 5  
 cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag 163  
 Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys  
 10 15 20  
 aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc 211  
 Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly  
 25 30 35  
 att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc 259  
 Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser  
 40 45 50  
 cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag 307  
 Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys  
 55 60 65  
 aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc 355  
 Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu  
 70 75 80 85  
 tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga 403  
 Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg  
 90 95 100  
 atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg 451  
 Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu  
 105 110 115  
 acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct 499  
 Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala  
 120 125 130  
 aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg 547  
 Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val  
 135 140 145  
 cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag 595  
 Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln  
 150 155 160 165  
 atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc 643  
 Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile  
 170 175 180

tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691  
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu  
                   185                                  190                                  195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740  
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr  
                   200                                  205                                  210

gttgaaacca ctg 753

<210> 1026

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1026

Met Ser Glu Asn Leu Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg  
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Ile Gln Met Ile Lys Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu  
                   20                                  25                                  30

Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu  
                   35                                  40                                  45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val  
                   50                                  55                                  60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg  
   65                                  70                                  75                                  80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp  
                   85                                  90                                  95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala  
                   100                                  105                                  110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala  
                   115                                  120                                  125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His  
                   130                                  135                                  140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val  
   145                                  150                                  155                                  160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser  
                   165                                  170                                  175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser  
                   180                                  185                                  190

Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu  
                   195                                  200                                  205

Val Thr  
   210

<210> 1027



<211> 1158  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1135)  
 <223> RXN02772

<400> 1027

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agatcctcag tagaaggatc gaaagaaagg cggcaggaaa atg agt ctg gag cgc 115
                                         Met Ser Leu Glu Arg
                                         1      5

aac aca caa aaa tct tcc atg ggt gtg cga agc atg tca gcc agg ctt 163
Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
                        10                        15                        20

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 211
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                        25                        30                        35

ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
                        40                        45                        50

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
                        55                        60                        65

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                        70                        75                        80                        85

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 403
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                        90                        95                        100

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 451
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                        105                        110                        115

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 499
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                        120                        125                        130

aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 547
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                        135                        140                        145

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 595
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                        150                        155                        160                        165

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 643
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
                        170                        175                        180

ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala  
 185 190 195  
 cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 739  
 Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu  
 200 205 210  
 gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 787  
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val  
 215 220 225  
 cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 835  
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu  
 230 235 240 245  
 att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 883  
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala  
 250 255 260  
 gaa gtg ctt ggt cga cca aag cac tac tgg tct atc tat caa aag atg 931  
 Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met  
 265 270 275  
 atc gtt cgc ggt cgt gat ttt gac gat att ttt gat ctt gtt ggc atc 979  
 Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile  
 280 285 290  
 cgc atc ctg gta gac aac gtg aac aac tgt gta cgc cgc cat cgg tgt  
 1027  
 Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val Arg Arg His Arg Cys  
 295 300 305  
 cgt gca ctc cct gtt caa tgc tct gcc tgg ccg att caa aga cta tat  
 1075  
 Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro Ile Gln Arg Leu Tyr  
 310 315 320 325  
 ttc agc ccc gcg ctt cgg tgt cta cca atc cct gca cac cac cgt gat  
 1123  
 Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro Ala His His Arg Asp  
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 1158  
 Gly Thr Trp Arg  
 345  
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 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 1028  
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 Met Ser Ala Arg Leu Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr  
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 Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro

35					40					45						
Arg	Ala	Asp	Val	Gln	Val	Leu	Glu	Arg	Ala	Tyr	Asp	Thr	Ala	Glu	Arg	
50					55					60						
Leu	His	Asp	Gly	Val	Ile	Arg	Lys	Ser	Gly	Asp	Pro	Tyr	Ile	Thr	His	
65					70					75					80	
Pro	Leu	Ala	Val	Ala	Thr	Ile	Ala	Ala	Glu	Ile	Gly	Met	Asp	Thr	Thr	
85					90					95						
Thr	Leu	Val	Ala	Ala	Leu	Leu	His	Asp	Thr	Val	Glu	Asp	Thr	Asp	Tyr	
100					105					110						
Ser	Leu	Asp	Asp	Leu	Thr	Arg	Asp	Phe	Gly	Glu	Glu	Val	Ala	Arg	Leu	
115					120					125						
Val	Asp	Gly	Val	Thr	Lys	Leu	Asp	Lys	Val	Ala	Leu	Gly	Ala	Ala	Ala	
130					135					140						
Glu	Ala	Glu	Thr	Ile	Arg	Lys	Met	Ile	Val	Ala	Met	Ser	Gln	Asp	Pro	
145					150					155					160	
Arg	Val	Leu	Val	Ile	Lys	Val	Ala	Asp	Arg	Leu	His	Asn	Met	Arg	Thr	
165					170					175						
Met	Arg	Phe	Leu	Pro	Pro	Glu	Lys	Gln	Ala	Lys	Lys	Ala	Arg	Gln	Thr	
180					185					190						
Leu	Glu	Val	Ile	Ala	Pro	Leu	Ala	His	Arg	Leu	Gly	Met	Ala	Ser	Val	
195					200					205						
Lys	Trp	Glu	Leu	Glu	Asp	Leu	Ser	Phe	Ala	Ile	Leu	Tyr	Pro	Lys	Lys	
210					215					220						
Tyr	Glu	Glu	Ile	Val	Arg	Leu	Val	Ala	Asp	Arg	Ala	Pro	Ser	Arg	Asp	
225					230					235					240	
Arg	Tyr	Leu	Lys	Glu	Ile	Ile	Asp	Gln	Val	Thr	Gly	Gly	Leu	Arg	Glu	
245					250					255						
Asn	Asn	Ile	Ala	Ala	Glu	Val	Leu	Gly	Arg	Pro	Lys	His	Tyr	Trp	Ser	
260					265					270						
Ile	Tyr	Gln	Lys	Met	Ile	Val	Arg	Gly	Arg	Asp	Phe	Asp	Asp	Ile	Phe	
275					280					285						
Asp	Leu	Val	Gly	Ile	Arg	Ile	Leu	Val	Asp	Asn	Val	Asn	Asn	Cys	Val	
290					295					300						
Arg	Arg	His	Arg	Cys	Arg	Ala	Leu	Pro	Val	Gln	Cys	Ser	Ala	Trp	Pro	
305					310					315					320	
Ile	Gln	Arg	Leu	Tyr	Phe	Ser	Pro	Ala	Leu	Arg	Cys	Leu	Pro	Ile	Pro	
325					330					335						
Ala	His	His	Arg	Asp	Gly	Thr	Trp	Arg								
340					345											

&lt;210&gt; 1029

<211> 903  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(880)  
 <223> FRXA02772

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 Met Ser Ala Arg Leu  
 1 5

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 163  
 Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp  
 10 15 20

ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 211  
 Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln  
 25 30 35

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 259  
 Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val  
 40 45 50

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 307  
 Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala  
 55 60 65

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 355  
 Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala  
 70 75 80 85

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 403  
 Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu  
 90 95 100

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 451  
 Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr  
 105 110 115

aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 499  
 Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile  
 120 125 130

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 547  
 Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile  
 135 140 145

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 595  
 Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro  
 150 155 160 165

ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 643  
 Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala  
 170 175 180

cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 691

Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu  
 185 190 195

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 739  
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val  
 200 205 210

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787  
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu  
 215 220 225

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835  
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala  
 230 235 240 245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880  
 Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu Ser Phe Lys Arg  
 250 255 260

tgatcggtcg cggtcgtgat ttt 903

&lt;210&gt; 1030

&lt;211&gt; 260

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1030

Met Ser Ala Arg Leu Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr  
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Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro  
 20 25 30

Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg  
 35 40 45

Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His  
 50 55 60

Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr  
 65 70 75 80

Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr  
 85 90 95

Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu  
 100 105 110

Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala  
 115 120 125

Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro  
 130 135 140

Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr  
 145 150 155 160

Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr  
 165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val  
 180 185 190  
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys  
 195 200 205  
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp  
 210 215 220  
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu  
 225 230 235 240  
 Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu  
 245 250 255  
 Ser Phe Lys Arg  
 260

<210> 1031  
 <211> 262  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(262)  
 <223> FRXA02773

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 tgcttggtcg nccnaagcac tctgggtcttt ctttcaaaag atg atc gtt cgc ggt 115  
 Met Ile Val Arg Gly  
 1 5  
 cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163  
 Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa  
 10 15 20  
 gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc ccn 211  
 Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro  
 25 30 35  
 gtn caa tgc tct gnc tgg ncg ntt caa aga cta tat ttc agc ccc gcg 259  
 Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu Tyr Phe Ser Pro Ala  
 40 45 50  
 ctt 262  
 Leu

<210> 1032  
 <211> 54  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1032  
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 1 5 10 15

Ile Arg Xaa Leu Xaa Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg  
                   20                  25                  30

Cys Arg Ala Leu Pro Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu  
                   35                  40                  45

Tyr Phe Ser Pro Ala Leu  
                   50

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(631)  
 <223> RXA01835

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ttctctgcgtg aatacacttt ccccgcgccct tcgcaaagct atg aat act gcc gcg 115  
   Met Asn Thr Ala Ala  
   1                  5

tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163  
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val  
                                   10                  15                  20

agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211  
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp  
                   25                  30                  35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259  
 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val  
                   40                  45                  50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307  
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg  
                   55                  60                  65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355  
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp  
                   70                  75                  80                  85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403  
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser  
                                   90                  95                  100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451  
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met  
                   105                  110                  115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499  
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg  
                   120                  125                  130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547

Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr  
 135 140 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595  
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu  
 150 155 160 165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641  
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala  
 170 175

gcggcgctcga taa 654

<210> 1034  
 <211> 177  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 1034  
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 1 5 10 15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala  
 20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp  
 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala  
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln  
 65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu  
 85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys  
 100 105 110

Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu  
 115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp  
 130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu  
 145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser  
 165 170 175

Ala

<210> 1035  
 <211> 1395  
 <212> DNA  
 <213> *Corynebacterium glutamicum*



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1372)

&lt;223&gt; RXA01483

&lt;400&gt; 1035

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gcgtgcacgc catgagcaac ttcggaggct gaaaaagtag atg tac ccc tat tcc 115
                Met Tyr Pro Tyr Ser
                1                    5

gac gca gac gct ttt cga cgc cag cct gag cgc gcc aag tcc agc caa 163
Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg Ala Lys Ser Ser Gln
                10                    15                    20

ctg cgt acc agc gcc gta gac acc cgc agc gcg ttc gcc cgc gac cgg 211
Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
                25                    30                    35

gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
                40                    45                    50

caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
                55                    60                    65

cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
                70                    75                    80                    85

gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
                90                    95                    100

ggg cat ccg ccg tat gga cac aac ggt gaa aac gcg ttg aat gaa gtt 451
Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
                105                    110                    115

gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
                120                    125                    130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
                135                    140                    145

ggg ctg aac ttg tcg cgg gct gct ctt gat gct gca tgt aag tat ccg 595
Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
                150                    155                    160                    165

tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct 643
Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
                170                    175                    180

tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
                185                    190                    195

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gat ctt cgc cca ccg atc gaa gcg cag gtc atg gac ttt tct gat gac 739  
 Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met Asp Phe Ser Asp Asp  
 200 205 210

att gcc tac tcg gtg cac gat gtg gaa gac ggt att gta tcc ggg cgt 787  
 Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg  
 215 220 225

atc gac tta aaa gtg ctg tgg gac ctg gtt gaa tta gca gct ttg gca 835  
 Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala  
 230 235 240 245

gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag 883  
 Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu  
 250 255 260

ggt gca gca tcg ttg cgg gaa ctt ccg gtg gtg gct gcc gct gcg gat 931  
 Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Ala Asp  
 265 270 275

ttt gat ttc tca ctg cgt tcc tac gct gcg ctg aag gcg atg act tca 979  
 Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser  
 280 285 290

gaa cta gtg gga aga tac gtt ggc tct acc atc gag tca aca aag aaa  
 1027  
 Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys  
 295 300 305

aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att  
 1075  
 Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile  
 310 315 320 325

cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt  
 1123  
 Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val  
 330 335 340

ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa  
 1171  
 Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln  
 345 350 355

cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg  
 1219  
 Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro  
 360 365 370

gga tcg ttg gat ccg atg tat cgc cag tgg ttt att gaa gcg gat tca  
 1267  
 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser  
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg  
 1315  
 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr  
 390 395 400 405

gag tct cgt ctg gaa cgc ctt gcc cgg aat gct gct gac atc tca gga  
 1363

Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala Ala Asp Ile Ser Gly  
 410 415 420

ttt ttg gga taattggta gagcagcagt aag  
 1395  
 Phe Leu Gly

<210> 1036

<211> 424

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1036

Met Tyr Pro Tyr Ser Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg  
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Ala Lys Ser Ser Gln Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala  
 20 25 30

Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg  
 35 40 45

Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro  
 50 55 60

Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly  
 65 70 75 80

Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly  
 85 90 95

Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn  
 100 105 110

Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala  
 115 120 125

Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp  
 130 135 140

Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala  
 145 150 155 160

Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn  
 165 170 175

Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile  
 180 185 190

Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met  
 195 200 205

Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly  
 210 215 220

Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu  
 225 230 235 240

Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro

	245		250		255
Ala Glu Leu	Ile Glu Gly	Ala Ala Ser	Leu Arg Glu	Leu Pro Val	Val
	260		265		270
Ala Ala Ala	Ala Asp Phe	Asp Phe Ser	Leu Arg Ser	Tyr Ala Ala	Leu
	275		280		285
Lys Ala Met	Thr Ser Glu	Leu Val Gly	Arg Tyr Val	Gly Ser Thr	Ile
	290		295		300
Glu Ser Thr	Lys Lys Thr	His Ala Gly	Ile Asp Val	Gly Arg Met	His
	305		310		315
Gly Asp Leu	Ile Ile Pro	Glu Thr Ala	Ala Ser Glu	Val Lys Leu	Leu
	325		330		335
Lys Thr Leu	Ala Val Leu	Tyr Val Met	Asp Asp Pro	Gly His Leu	Ala
	340		345		350
Arg Gln Asn	Arg Gln Arg	Asp Arg Ile	Phe Arg Val	Phe Asp Tyr	Leu
	355		360		365
Val Leu Gly	Ala Pro Gly	Ser Leu Asp	Pro Met Tyr	Arg Gln Trp	Phe
	370		375		380
Ile Glu Ala	Asp Ser Glu	Ser Glu Gln	Ile Arg Val	Ile Val Asp	Gln
	385		390		400
Ile Ala Ser	Met Thr Glu	Ser Arg Leu	Glu Arg Leu	Ala Arg Asn	Ala
	405		410		415
Ala Asp Ile	Ser Gly Phe	Leu Gly			
	420				

<210> 1037  
 <211> 1131  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
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 <222> (101)..(1108)  
 <223> RXN01027

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gaactgtgtg	caccacaacg	cggaaggtga	atcgcaccca	atg gca aat aag aac	115
				Met Ala Asn Lys Asn	
				1 5	

aat aag cct	cat gag gtg	gac aaa gac	caa gat tca	gcc atg ctg	atc	163
Asn Lys Pro	His Glu Val	Asp Lys Asp	Gln Asp Ser	Ala Met Leu	Ile	
	10		15		20	

aac ggt cgc	ctg caa cag	atc ccg gcg	cgt ccc act	gag gaa ttc	acc	211
Asn Gly Arg	Leu Gln Gln	Ile Pro Ala	Arg Pro Thr	Glu Glu Phe	Thr	
	25		30		35	

cg	cc	act	ctt	gca	gca	ggt	gca	gta	ctg	tgg	cg	gg	gac	atc	acc	259
Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp	Arg	Gly	Asp	Ile	Thr	
		40					45					50				
aac	ccg	gac	agc	atc	gag	gtc	gct	gtc	atc	cac	cg	ccg	cac	tat	gat	307
Asn	Pro	Asp	Ser	Ile	Glu	Val	Ala	Val	Ile	His	Arg	Pro	His	Tyr	Asp	
	55					60				65						
gac	tgg	tcc	ctg	gcc	aag	ggc	aaa	gtc	gat	ccc	ggc	gag	tct	att	ccg	355
Asp	Trp	Ser	Leu	Ala	Lys	Gly	Lys	Val	Asp	Pro	Gly	Glu	Ser	Ile	Pro	
70					75					80					85	
aca	acc	gcg	gcc	cgt	gaa	atc	ctt	gaa	gaa	act	ggc	tac	gac	atc	cgt	403
Thr	Thr	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Tyr	Asp	Ile	Arg	
				90				95						100		
ctg	ggc	aag	ctg	atc	ggc	aag	gtt	act	tac	cct	gtg	ctc	gac	cga	acc	451
Leu	Gly	Lys	Leu	Ile	Gly	Lys	Val	Thr	Tyr	Pro	Val	Leu	Asp	Arg	Thr	
			105					110					115			
aaa	gtg	gtc	tac	tac	tgg	act	gcc	cag	gtt	ctt	ggg	gga	gag	ttt	gtc	499
Lys	Val	Val	Tyr	Tyr	Trp	Thr	Ala	Gln	Val	Leu	Gly	Gly	Glu	Phe	Val	
		120					125					130				
ccc	aac	gat	gaa	gtt	gat	gaa	atc	cgt	tgg	ctg	tct	gtt	gat	gaa	gca	547
Pro	Asn	Asp	Glu	Val	Asp	Glu	Ile	Arg	Trp	Leu	Ser	Val	Asp	Glu	Ala	
	135					140					145					
tgc	gag	ttg	ctc	agc	tac	caa	gta	gat	acc	gaa	gtt	ctg	gcc	aag	gca	595
Cys	Glu	Leu	Leu	Ser	Tyr	Gln	Val	Asp	Thr	Glu	Val	Leu	Ala	Lys	Ala	
150					155					160					165	
gca	aag	cgt	ttc	cg	act	cct	tcc	acc	act	cgg	gtg	ctg	tat	gtt	cg	643
Ala	Lys	Arg	Phe	Arg	Thr	Pro	Ser	Thr	Thr	Arg	Val	Leu	Tyr	Val	Arg	
				170					175					180		
cat	gct	cat	gca	cat	ggg	cg	caa	acc	tgg	ggg	ggc	gac	gac	aat	aag	691
His	Ala	His	Ala	His	Gly	Arg	Gln	Thr	Trp	Gly	Gly	Asp	Asp	Asn	Lys	
			185				190						195			
cg	cca	ttg	gac	aaa	aag	ggg	cgt	cga	caa	gca	gaa	atg	ctc	gta	ccc	739
Arg	Pro	Leu	Asp	Lys	Lys	Gly	Arg	Arg	Gln	Ala	Glu	Met	Leu	Val	Pro	
		200				205						210				
atg	ttg	ttg	ccc	ttc	aaa	ccc	acc	gca	att	tac	tcg	gcg	gtg	ccc	gat	787
Met	Leu	Leu	Pro	Phe	Lys	Pro	Thr	Ala	Ile	Tyr	Ser	Ala	Val	Pro	Asp	
	215					220					225					
cg	tgc	caa	gcc	acc	gcg	ctc	ccc	ctt	gcc	gat	gag	ctc	ggc	ctc	gac	835
Arg	Cys	Gln	Ala	Thr	Ala	Leu	Pro	Leu	Ala	Asp	Glu	Leu	Gly	Leu	Asp	
230					235					240				245		
gtg	tcc	gtc	aac	cga	ctg	ttc	ggc	gac	gac	gcc	tgg	gaa	acc	gat	ccc	883
Val	Ser	Val	Asn	Arg	Leu	Phe	Gly	Asp	Asp	Ala	Trp	Glu	Thr	Asp	Pro	
				250				255						260		
gag	gcc	tgc	aag	aag	cg	ttc	acc	gac	gtg	gtc	gcg	caa	ggg	ggc	gtg	931
Glu	Ala	Cys	Lys	Lys	Arg	Phe	Thr	Asp	Val	Val	Ala	Gln	Gly	Gly	Val	
			265				270						275			
ccg	atg	atc	gtt	ggg	cag	ggc	gac	atc	att	ccg	gaa	atg	atc	aaa	tgg	979

Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp  
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa  
 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys  
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc  
 1075

Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly  
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg tttaaggcct  
 1128

Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 330 335

cca  
 1131

<210> 1038

<211> 336

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1038

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp  
 1 5 10 15

Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro  
 20 25 30

Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp  
 35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr  
 210 215 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp  
 225 230 235 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala  
 245 250 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val  
 260 265 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro  
 275 280 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu  
 290 295 300

Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp  
 305 310 315 320

Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 325 330 335

&lt;210&gt; 1039

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(757)

&lt;223&gt; FRXA01024

&lt;400&gt; 1039

aatagatgga agtagttttt cattcactta tgtgcgcggtt tttaatctgg tttctaccaa 60

gaactgtgtg caccacaacg cggaagggtga atcgcaccca atg gca aat aag aac 115  
 Met Ala Asn Lys Asn  
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163  
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile  
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211  
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr  
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259  
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr

40	45	50	
aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat			307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp			
55	60	65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg			355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro			
70	75	80	85
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt			403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg			
90	95	100	
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc			451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr			
105	110	115	
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc			499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val			
120	125	130	
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca			547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala			
135	140	145	
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Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala			
150	155	160	165
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc			643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg			
170	175	180	
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag			691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys			
185	190	195	
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc			739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro			
200	205	210	
atg ttg ttg ccc ttc aaa			757
Met Leu Leu Pro Phe Lys			
215			

&lt;210&gt; 1040

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1040

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1				5					10					15	

Ser	Ala	Met	Leu	Ile	Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro
			20					25					30		

Thr	Glu	Glu	Phe	Thr	Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp
	35						40					45			



Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
 50 55 60  
 Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
 65 70 75 80  
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
 85 90 95  
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
 100 105 110  
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
 115 120 125  
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
 130 135 140  
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
 145 150 155 160  
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
 165 170 175  
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
 180 185 190  
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
 195 200 205  
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys  
 210 215

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 <223> FRXA01027

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 Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln  
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 ggt ggc gtg ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg 96  
 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
 20 25 30  
 atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144  
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
 35 40 45  
 aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192  
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
 50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234  
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
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taggagcgcg ttttaaggcct cca 257

<210> 1042

<211> 78

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1042

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Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
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Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
 35 40 45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
 50 55 60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
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<210> 1043

<211> 651

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01528

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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115  
 Val Asn Gln Ala Trp  
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163  
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu  
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211  
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp  
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259  
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly  
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307  
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

```

      55              60              65
aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac   355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
  70              75              80              85

ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg   403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
      90              95              100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat   451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
      105              110              115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg   499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
      120              125              130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag   547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
      135              140              145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg   595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
      150              155              160              165

aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaacccg 648
Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
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<210> 1044

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1044

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  1              5              10              15

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Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
      20              25              30

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Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
      35              40              45

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Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
      50              55              60

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Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
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Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
      85              90              95

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Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
      100              105              110

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His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu

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115	120	125
Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu		
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145	150	155
Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg		
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 Met Ser Phe Gln Leu  
 1 5  
 gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163  
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser  
 10 15 20  
 ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211  
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys  
 25 30 35  
 cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259  
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala  
 40 45 50  
 agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307  
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala  
 55 60 65  
 att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355  
 ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala  
 70 75 80 85  
 gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403  
 Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr  
 90 95 100  
 cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451  
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr  
 105 110 115  
 tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499

Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln  
           120                  125                  130  
 gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541  
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 <212> PRT  
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 Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser  
           20                  25                  30  
 Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala  
           35                  40                  45  
 Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu  
           50                  55                  60  
 His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val  
           65                  70                  75                  80  
 Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe  
                   85                  90                  95  
 Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln  
           100                  105                  110  
 Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu  
           115                  120                  125  
 Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser  
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 Asn Pro Ala  
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   Met Glu Glu Pro Ser  
   1                  5

ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag	163
Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys	
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ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat	211
Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp	
25 30 35	
ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac	259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn	
40 45 50	
gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc	307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala	
55 60 65	
ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt	355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg	
70 75 80 85	
ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt	403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu	
90 95 100	
gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa	451
Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln	
105 110 115	
tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac	499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr	
120 125 130	
aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc	547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr	
135 140 145	
atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg	595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu	
150 155 160 165	
gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg	643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala	
170 175 180	
tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc	691
Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val	
185 190 195	
ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc	739
Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg	
200 205 210	
gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg	787
Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp	
215 220 225	
ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct	835
Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala	
230 235 240 245	

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883  
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu  
                   250                  255                  260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931  
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val  
                   265                  270                  275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979  
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys  
                   280                  285                  290

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 1002

<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

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                   20                  25                  30

Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala  
                   35                  40                  45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly  
                   50                  55                  60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val  
                   65                  70                  75                  80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp  
                   85                  90                  95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala  
                   100                  105                  110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val  
                   115                  120                  125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met  
                   130                  135                  140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu  
                   145                  150                  155                  160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val  
                   165                  170                  175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser  
                   180                  185                  190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu  
                   195                  200                  205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr  
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg  
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala  
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly  
 260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln  
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Gln Lys Asp Glu Lys  
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 Val Gln Lys Asp Ser  
 1 5

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 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
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att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355  
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403  
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn  
 90 95 100

tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451



Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro		
			105					110					115				
gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggc	499	
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly		
		120					125					130					
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547	
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp		
		135				140						145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595	
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro		
150					155					160					165		
ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643	
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile		
			170						175					180			
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg	691	
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu		
			185					190					195				
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739	
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met		
		200					205					210					
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggc	cta	tcc	ttg	cca	787	
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro		
		215				220					225						
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggc	acg	gaa	835	
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu		
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Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile		
				250					255					260			
acc	gaa	gcc	ggc	gac	ggc	att	acc	att	atc	aac	atc	ggc	gtg	ggc	cca	931	
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro		
			265				270						275				
tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979	
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu		
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gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc		
1027																	
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg		
		295				300					305						
atc	ggc	gac	ctc	atc	ctt	ggc	aac	gcc	tac	cag	cgc	gaa	gac	cac	att		
1075																	
Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln	Arg	Glu	Asp	His	Ile		
310					315					320				325			
ctg	aat	acc	cgc	atc	cca	ctt	ggc	aat	ccg	atc	ccg	gca	ata	cca	gaa		
1123																	
Leu	Asn	Thr	Arg	Ile	Pro	Leu	Gly	Asn	Pro	Ile	Pro	Ala	Ile	Pro	Glu		
				330					335					340			

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc  
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga  
1545

Thr Leu Gly Glu Val Pro Phe Arg  
470 475

<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp  
1 5 10 15

Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala  
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
 50 55 60  
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
 65 70 75 80  
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
 85 90 95  
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
 100 105 110  
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
 115 120 125  
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
 130 135 140  
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
 145 150 155 160  
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
 165 170 175  
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
 180 185 190  
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
 195 200 205  
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
 210 215 220  
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
 325 330 335  
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser  
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn  
 370 375 380  
 Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr  
 385 390 395 400  
 Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu  
 405 410 415  
 Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln  
 420 425 430  
 Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala  
 435 440 445  
 Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr  
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 Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg  
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 <213> *Corynebacterium glutamicum*

<220>  
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 <222> (101)..(1168)  
 <223> FRXA02281

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 cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115  
 Val Gln Lys Asp Ser  
 1 5  
 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
 10 15 20  
 att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35  
 aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50  
 gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65  
 tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355  
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
 70 75 80 85  
 gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403  
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn

90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg			451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro			
105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt			499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly			
120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac			547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp			
135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg			595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro			
150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc			643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile			
170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg			691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu			
185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg			739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met			
200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca			787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro			
215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa			835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu			
230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc			883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile			
250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca			931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro			
265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa			979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu			
280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc			
1027			
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg			
295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att			
1075			
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile			
310	315	320	325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc  
1168

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser  
345 350 355

tagtattcta tagtgtcacc taa  
1191

<210> 1052

<211> 356

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1052

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp  
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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala  
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
 325 330 335  
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser  
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 <211> 1146  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1123)  
 <223> RXN01240

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 Met Ser Asp Asn Thr  
 1 5  
 ctc tcc caa ttt ggc agt tac tac cac gaa ttc cga cgt gcc cat ccc 163  
 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro  
 10 15 20  
 atg gcc gac gtc gaa ttc ctc cta gca att gaa gaa tta ctt acg gac 211  
 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp  
 25 30 35  
 ggt ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259  
 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser  
 40 45 50  
 agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307  
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile  
 55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc	355
Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile	
70 75 80 85	
acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa	403
Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln	
90 95 100	
gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc	451
Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg	
105 110 115	
atc tca ggc ggc ttt ggt tac ggc tcc cac cac ctg att ctg gaa gtc	499
Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val	
120 125 130	
gat gac acc tcc gat gac ctc cag gac tac aaa ggc ctc gtc ttt gaa	547
Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu	
135 140 145	
gtt cag gtg cgc acc gtg ctg caa cac gcc tgg gca gag ttc gaa cac	595
Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His	
150 155 160 165	
gat atc cgc tat aaa cgc gcc gat gtg tcc aac cca gaa gac ttc agc	643
Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser	
170 175 180	
gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta	691
Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu	
185 190 195	
gcg gac caa caa ttc gac caa atc gcc gca ctc aaa gaa acc agc cga	739
Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg	
200 205 210	
gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt	787
Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val	
215 220 225	
ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac	835
Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn	
230 235 240 245	
tac cgc ttc ctc gaa gac atc ctg gtg gcc aac tcc att acc tct gtg	883
Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val	
250 255 260	
gtg cag ctg cgc gag ctg ctc aac ccc acc gac att gaa gtg ctg ttg	931
Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu	
265 270 275	
aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac	979
Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp	
280 285 290	
gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc	
1027	
Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val	
295 300 305	



gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa  
1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys  
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac  
1123

Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu Val Glu Pro Pro Asn  
330 335 340

taaagttccc ccaaagttag ccc  
1146

<210> 1054

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

Met Ser Asp Asn Thr Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe  
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Arg Arg Ala His Pro Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu  
20 25 30

Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg  
35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn  
50 55 60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met  
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala  
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys  
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His  
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys  
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp  
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn  
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala  
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu  
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

210	215	220
Thr Leu Pro Gly Val	Leu Ala Met Leu Ile	Gly Asn Arg Phe Pro Arg
225	230	235 240
Pro Arg Ser Thr Asn Tyr Arg Phe Leu	Glu Asp Ile Leu Val Ala Asn	
	245	250 255
Ser Ile Thr Ser Val Val Gln Leu Arg	Glu Leu Leu Asn Pro Thr Asp	
	260	265 270
Ile Glu Val Leu Leu Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln		
	275	280 285
Ile Arg Ile Ile Asp Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His		
	290	295 300
Ile Asp Ala Thr Val Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg		
	305	310 315 320
His Arg Gln Leu Lys Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu		
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Val Glu Pro Pro Asn		
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1234)  
 <223> RXN02008

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 Val Tyr Ala Ala Ile  
 1 5  
 ggt gtc gtg cac tcc ctg ttc aat gct ctg cct ggc cga ttc aaa gac 163  
 Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp  
 10 15 20  
 tat att tca gcc ccg cgc ttc ggt gtc tac caa tcc ctg cac acc acc 211  
 Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr  
 25 30 35  
 gtg atg gga cct ggc ggt aag cct ctg gaa gtt cag gca cgt acc cac 259  
 Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His  
 40 45 50  
 gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307  
 Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala Ala His Trp Arg Tyr  
 55 60 65  
 aaa gaa acc aaa ggc agc cac agt ggc gag caa gcc gaa gtg gat caa 355

Lys	Glu	Thr	Lys	Gly	Ser	His	Ser	Gly	Glu	Gln	Ala	Glu	Val	Asp	Gln			
70					75					80					85			
atg	gcg	tgg	atg	cgc	caa	ctt	ctg	gac	tgg	caa	aaa	gaa	gca	gcc	gac		403	
Met	Ala	Trp	Met	Arg	Gln	Leu	Leu	Asp	Trp	Gln	Lys	Glu	Ala	Ala	Asp			
				90					95					100				
ccc	aac	gag	ttc	ctg	gac	agc	ctg	cgc	tac	gat	ctg	act	tcc	aag	cag		451	
Pro	Asn	Glu	Phe	Leu	Asp	Ser	Leu	Arg	Tyr	Asp	Leu	Thr	Ser	Lys	Gln			
			105					110					115					
atc	ttc	gtg	ttc	aca	ccc	aaa	ggg	gat	gtg	gtc	aac	ctg	ccg	gtg	aac		499	
Ile	Phe	Val	Phe	Thr	Pro	Lys	Gly	Asp	Val	Val	Asn	Leu	Pro	Val	Asn			
		120					125					130						
tcc	acc	ccg	gtg	gac	ttc	gcc	tac	gcg	gtg	cac	acc	gaa	gtg	ggg	cac		547	
Ser	Thr	Pro	Val	Asp	Phe	Ala	Tyr	Ala	Val	His	Thr	Glu	Val	Gly	His			
		135				140					145							
cgc	tgc	atc	ggc	gcc	aaa	atc	aac	ggc	aaa	ctg	gtc	gct	ttg	gaa	acg		595	
Arg	Cys	Ile	Gly	Ala	Lys	Ile	Asn	Gly	Lys	Leu	Val	Ala	Leu	Glu	Thr			
150					155					160					165			
aaa	ctc	aaa	tcc	ggc	gat	cgt	ggt	gaa	gtc	ttt	acc	tcc	aag	gac	caa		643	
Lys	Leu	Lys	Ser	Gly	Asp	Arg	Val	Glu	Val	Phe	Thr	Ser	Lys	Asp	Gln			
				170					175					180				
aac	gct	ggc	cca	agt	agg	gga	tgg	caa	gaa	ttt	ggt	gtc	tca	cct	cgt		691	
Asn	Ala	Gly	Pro	Ser	Arg	Gly	Trp	Gln	Glu	Phe	Val	Val	Ser	Pro	Arg			
			185					190					195					
gca	aag	gcc	aag	att	cgc	cag	tgg	ttt	gcc	aag	gaa	cga	cgc	gaa	gaa		739	
Ala	Lys	Ala	Lys	Ile	Arg	Gln	Trp	Phe	Ala	Lys	Glu	Arg	Arg	Glu	Glu			
		200					205					210						
tac	cta	gaa	gcc	gga	cgc	gat	gcg	ctg	gca	gca	ggt	att	cag	cgt	ggc		787	
Tyr	Leu	Glu	Ala	Gly	Arg	Asp	Ala	Leu	Ala	Ala	Val	Ile	Gln	Arg	Gly			
		215				220					225							
ggc	ctg	cca	atg	cac	cgc	ttg	ttc	acc	gcg	tcc	tcc	atg	aag	acg	gtg		835	
Gly	Leu	Pro	Met	His	Arg	Leu	Phe	Thr	Ala	Ser	Ser	Met	Lys	Thr	Val			
230					235					240					245			
gca	aca	gag	ctg	cac	tac	cca	gat	gta	gat	gcg	ctc	tac	aca	gcc	atc		883	
Ala	Thr	Glu	Leu	His	Tyr	Pro	Asp	Val	Asp	Ala	Leu	Tyr	Thr	Ala	Ile			
				250					255					260				
ggc	tcc	ggt	tct	gta	tct	gcg	caa	cac	gta	gtc	aac	cgt	ctc	atg	gct		931	
Gly	Ser	Gly	Ser	Val	Ser	Ala	Gln	His	Val	Val	Asn	Arg	Leu	Met	Ala			
			265				270						275					
atc	ttt	ggt	gac	gaa	gaa	gat	gcc	gaa	gac	gca	ttg	ggt	gca	cgc	acc		979	
Ile	Phe	Gly	Asp	Glu	Glu	Asp	Ala	Glu	Asp	Ala	Leu	Val	Ala	Arg	Thr			
		280					285					290						
cca	ttc	agc	gag	ctg	gtc	aac	tcc	cgt	gcc	acc	acg	gaa	agc	agc	acc		1027	
Pro	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr	Thr	Glu	Ser	Ser	Thr			
		295				300					305							

ggc atc ctg gtc gaa ggc agc cca gat gtc atg gct aag ctc gct aaa  
1075

Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met Ala Lys Leu Ala Lys  
310 315 320 325

tgc tgt atg cca gtg cca gga gat gaa atc ttt gga ttc gtc acc cgt  
1123

Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe Gly Phe Val Thr Arg  
330 335 340

ggg ggc ggt gtc tcc gta cac cga aca gac tgc acg aat gtg gaa aag  
1171

Gly Gly Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Val Glu Lys  
345 350 355

ctc aaa gaa gag cca gaa cgc att gtc tcc gtc tcc tgg gct tcg gaa  
1219

Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val Ser Trp Ala Ser Glu  
360 365 370

ggg caa ggt tca gta  
1234

Gly Gln Gly Ser Val  
375

<210> 1056

<211> 378

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1056

Val Tyr Ala Ala Ile Gly Val Val His Ser Leu Phe Asn Ala Leu Pro  
1 5 10 15

Gly Arg Phe Lys Asp Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln  
20 25 30

Ser Leu His Thr Thr Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val  
35 40 45

Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala  
50 55 60

Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln  
65 70 75 80

Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln  
85 90 95

Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp  
100 105 110

Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val  
115 120 125

Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His  
130 135 140

Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu  
145 150 155 160

Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe  
 165 170 175  
 Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe  
 180 185 190  
 Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys  
 195 200 205  
 Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala  
 210 215 220  
 Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser  
 225 230 235 240  
 Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala  
 245 250 255  
 Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val  
 260 265 270  
 Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala  
 275 280 285  
 Leu Val Ala Arg Thr Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr  
 290 295 300  
 Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met  
 305 310 315 320  
 Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe  
 325 330 335  
 Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys  
 340 345 350  
 Thr Asn Val Glu Lys Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val  
 355 360 365  
 Ser Trp Ala Ser Glu Gly Gln Gly Ser Val  
 370 375

&lt;210&gt; 1057

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1036)

&lt;223&gt; RXN01940

&lt;400&gt; 1057

ccagaatcaa tcaccgatac agtggcagcc aaagtccagg ctgaagaagc cgctcaagcc 60

gccagctaaa tccacaaact gaactaagga gttttaccct atg acc acc aag atc 115

Met Thr Thr Lys Ile

1

5

atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc	163
Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu	
10 15 20	
gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc	211
Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly	
25 30 35	
ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc	259
Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala	
40 45 50	
acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca	307
Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro	
55 60 65	
ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc	355
Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly	
70 75 80 85	
atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa	403
Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu	
90 95 100	
gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag	451
Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu	
105 110 115	
ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg	499
Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala	
120 125 130	
ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt	547
Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val	
135 140 145	
gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct	595
Val Leu Met Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala	
150 155 160 165	
gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac	643
Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn	
170 175 180	
gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg	691
Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala	
185 190 195	
ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac	739
Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp	
200 205 210	
gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac	787
Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr	
215 220 225	
cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct	835
Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala	
230 235 240 245	
gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca	883

Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro  
 250 255 260  
 ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931  
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala  
 265 270 275  
 gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979  
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val  
 280 285 290  
 gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag  
 1027  
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys  
 295 300 305  
 cgc atc gga tagacctgtt cacaagggttg tta  
 1059  
 Arg Ile Gly  
 310  
  
 <210> 1058  
 <211> 312  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 1058  
 Met Thr Thr Lys Ile Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala  
 1 5 10 15  
 Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly  
 20 25 30  
 Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn  
 35 40 45  
 Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg  
 50 55 60  
 Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile  
 65 70 75 80  
 His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro  
 85 90 95  
 Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr  
 100 105 110  
 Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro  
 115 120 125  
 Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu  
 130 135 140  
 Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn  
 145 150 155 160  
 Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala  
 165 170 175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp  
 180 185 190  
 Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn  
 195 200 205  
 Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala  
 210 215 220  
 Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val  
 225 230 235 240  
 His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr  
 245 250 255  
 Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr  
 260 265 270  
 Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr  
 275 280 285  
 Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val  
 290 295 300  
 Ile Asp Ala Val Lys Arg Ile Gly  
 305 310

&lt;210&gt; 1059

&lt;211&gt; 602

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(579)

&lt;223&gt; FRXA01940

&lt;400&gt; 1059

aga gta acg ctt gtt tcc acc ggg cca ctg acc aac atc gcg ctg gca	48
Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala	
1 5 10 15	
gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc	96
Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu	
20 25 30	
atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc	144
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe	
35 40 45	
aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag	192
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys	
50 55 60	
tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca	240
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala	
65 70 75 80	
aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc	288
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala	



85	90	95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac			336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp			
100	105	110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca			384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala			
115	120	125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat			432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp			
130	135	140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc			480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe			
145	150	155	160
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg			528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu			
165	170	175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc			576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile			
180	185	190	
gga tagacctgtt cacaagggttg tta			602
Gly			

&lt;210&gt; 1060

&lt;211&gt; 193

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1060

Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala	
1	15

Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu	
20	30

Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe	
35	45

Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys	
50	60

Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala	
65	80

Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala	
85	95

Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp	
100	110

Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala	
115	125

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp  
 130 135 140  
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe  
 145 150 155 160  
 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu  
 165 170 175  
 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile  
 180 185 190

Gly

<210> 1061  
 <211> 1026  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1003)  
 <223> RXA02559

<400> 1061  
 ttagtcctct atggcagcaa gcctgccaga ggagcctatc cagcactaga ccccaactag 60  
 aacccaaccc caaaaccaga aaacactaag ctcgtgagac atg att cct gtt ctc 115  
 Met Ile Pro Val Leu  
 1 5  
 atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163  
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu  
 10 15 20  
 gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211  
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr  
 25 30 35  
 acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259  
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp  
 40 45 50  
 gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307  
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln  
 55 60 65  
 cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355  
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly  
 70 75 80 85  
 gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403  
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu  
 90 95 100  
 ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451  
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr  
 105 110 115

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aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499
Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro
      120                      125                      130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547
Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn
      135                      140                      145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595
Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala
      150                      155                      160                      165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643
Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu
      170                      175                      180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691
Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu
      185                      190                      195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739
Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met
      200                      205                      210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787
Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu
      215                      220                      225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835
Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile
      230                      235                      240                      245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883
Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro
      250                      255                      260

ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931
Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys
      265                      270                      275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979
Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His
      280                      285                      290

gcg gaa ctt cta aga gca gtg gaa tgaaataatc cgggtgctgat gca
1026
Ala Glu Leu Leu Arg Ala Val Glu
      295                      300

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&lt;210&gt; 1062

&lt;211&gt; 301

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1062

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Met Ile Pro Val Leu Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu
  1           5           10           15

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Ala Leu Ile Tyr Leu Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu
      20           25           30

```

Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala  
           35                          40                          45  
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro  
           50                          55                          60  
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr  
           65                          70                          75                          80  
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His  
                           85                          90                          95  
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu  
                           100                          105                          110  
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu  
                           115                          120                          125  
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr  
           130                          135                          140  
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val  
           145                          150                          155                          160  
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile  
                           165                          170                          175  
 Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp  
                           180                          185                          190  
 Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu  
                           195                          200                          205  
 His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln  
           210                          215                          220  
 Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile  
           225                          230                          235                          240  
 Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val  
                           245                          250                          255  
 Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg  
                           260                          265                          270  
 Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp  
                           275                          280                          285  
 Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu  
           290                          295                          300

&lt;210&gt; 1063

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1027)

&lt;223&gt; RXA02497

&lt;400&gt; 1063

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tcgatgccgc cgctggcgaa gactcgggga aacctaaaaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
Val Arg Leu Gly Val
1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
200 205 210

```

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cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
    215                220                225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835
His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
230                235                240                245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
                250                255                260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
                265                270                275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
    280                285                290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag
1027
Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
    295                300                305

taacatttac ccggaagga gtt
1050

```

<210> 1064  
 <211> 309  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 1064
Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
  1                5                10                15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
    20                25                30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
    35                40                45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
    50                55                60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
    65                70                75                80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
    85                90                95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
    100                105                110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
    115                120                125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
    130                135                140

```

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly  
 145 150 155 160  
 Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg  
 165 170 175  
 Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu  
 180 185 190  
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly  
 195 200 205  
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro  
 210 215 220  
 Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu  
 225 230 235 240  
 Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala  
 245 250 255  
 Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly  
 260 265 270  
 Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val  
 275 280 285  
 Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile  
 290 295 300  
 Asp Lys Gly Leu Glu  
 305

<210> 1065  
 <211> 2226  
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 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2203)  
 <223> RXN01079

<400> 1065  
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 gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115  
 Met Asp Phe His Ala  
 1 5  
 ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
 10 15 20  
 gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
 25 30 35  
 cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu	
40 45 50	
gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc	307
Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe	
55 60 65	
cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc	355
Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg	
70 75 80 85	
ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg	403
Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu	
90 95 100	
aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc	451
Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val	
105 110 115	
tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag	499
Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu	
120 125 130	
aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca	547
Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro	
135 140 145	
acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc	595
Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys	
150 155 160 165	
ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc	643
Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile	
170 175 180	
aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg	691
Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu	
185 190 195	
ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa aac	739
Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Asn	
200 205 210	
cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc	787
Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe	
215 220 225	
tcc tac gct aac cag ctg ggt gct cgt cag ggt gca ggt gct gtg tac	835
Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly Ala Gly Ala Val Tyr	
230 235 240 245	
ctc aac gct cac cac cca gat atc ctg tcc ttc ctg gat acc aag cgt	883
Leu Asn Ala His His Pro Asp Ile Leu Ser Phe Leu Asp Thr Lys Arg	
250 255 260	
gag aac gcc gat gag aag atc cgc atc aag acc ctg tcc ctg ggt gtt	931
Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr Leu Ser Leu Gly Val	
265 270 275	
gtg att ccg gac atc acc ttc gag ctg gct aag cgc aac gat gac atg	979
Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys Arg Asn Asp Asp Met	



280	285	290
tac ctg ttc tcc cca tac gat gtg gag cgc att tac ggc aag cct ttc 1027		
Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile Tyr Gly Lys Pro Phe 295 300 305		
gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac 1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp 310 315 320 325		
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg 1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu 330 335 340		
gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac 1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp 345 350 355		
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac 1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn 360 365 370		
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat 1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp 375 380 385		
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt 1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly 390 395 400 405		
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc 1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr 410 415 420		
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc 1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser 425 430 435		
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc 1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala 440 445 450		
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac 1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His 455 460 465		
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt 1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe 470 475 480 485		

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act  
1603

Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr  
490 495 500

gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc  
1651

Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr  
505 510 515

ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc  
1699

Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser  
520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc  
1747

Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr  
535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg  
1795

Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu  
550 555 560 565

ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac  
1843

Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr  
570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag  
1891

Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu  
585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac  
1939

Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His  
600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc  
1987

Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly  
615 620 625

tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac  
2035

Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp  
630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt  
2083

Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg  
650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc  
2131

Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr  
665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt  
2179

Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val  
680 685 690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatatc ccc  
2226

Asp Gly Cys Val Ser Cys Met Leu  
695 700

<210> 1066

<211> 701

<212> PRT

<213> Corynebacterium glutamicum

<400> 1066

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
1 5 10 15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu  
50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr  
65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr  
85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg  
100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp  
115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe  
130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly  
145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser  
165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly  
180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile  
195 200 205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu  
210 215 220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly  
225 230 235 240

Ala Gly Ala Val Tyr Leu Asn Ala His His Pro Asp Ile Leu Ser Phe  
 245 250 255  
 Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr  
 260 265 270  
 Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys  
 275 280 285  
 Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile  
 290 295 300  
 Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu  
 305 310 315 320  
 Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln  
 325 330 335  
 Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr  
 340 345 350  
 Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg  
 355 360 365  
 Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro  
 370 375 380  
 Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile  
 385 390 395 400  
 Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro  
 405 410 415  
 Asn Phe Glu Lys Thr Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val  
 420 425 430  
 Pro Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn  
 435 440 445  
 Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr  
 450 455 460  
 Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe  
 465 470 475 480  
 Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser  
 485 490 495  
 Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn  
 500 505 510  
 Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp  
 515 520 525  
 Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn  
 530 535 540  
 Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val  
 545 550 555 560

Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr  
                   565                                  570                  575

Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile  
                   580                                  585                  590

Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr  
                   595                                  600                  605

Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp  
                   610                                  615                  620

Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala  
                   625                                  630                  635                  640

Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp  
                   645                                  650                  655

Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg  
                   660                                  665                  670

Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu  
                   675                                  680                  685

Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu  
                   690                                  695                  700

&lt;210&gt; 1067

&lt;211&gt; 790

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(790)

&lt;223&gt; FRXA01079

&lt;400&gt; 1067

accttaaaac ttaatcaatc aatacaaagt tcacacctct ttgaaaggg acattccttt 60

gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115  
   Met Asp Phe His Ala  
   1                  5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
   Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
                   10                                  15                  20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
   Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
                   25                                  30                  35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259  
   Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu  
                   40                                  45                  50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307  
   Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe  
                   55                                  60                  65

cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355  
 Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg  
 70 75 80 85  
  
 ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403  
 Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu  
 90 95 100  
  
 aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451  
 Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val  
 105 110 115  
  
 tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499  
 Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu  
 120 125 130  
  
 aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547  
 Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro  
 135 140 145  
  
 acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595  
 Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys  
 150 155 160 165  
  
 ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643  
 Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile  
 170 175 180  
  
 aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691  
 Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu  
 185 190 195  
  
 ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739  
 Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile  
 200 205 210  
  
 cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787  
 Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe  
 215 220 225  
  
 tcc 790  
 Ser  
 230

&lt;210&gt; 1068

&lt;211&gt; 230

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1068

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
 1 5 10 15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
 20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
 35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

50                      55                      60  
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr  
 65                      70                      75                      80  
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr  
                     85                      90                      95  
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg  
                     100                      105                      110  
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp  
                     115                      120                      125  
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe  
                     130                      135                      140  
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly  
 145                      150                      155                      160  
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser  
                     165                      170                      175  
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly  
                     180                      185                      190  
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile  
                     195                      200                      205  
 Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu  
                     210                      215                      220  
 Leu Glu Asp Ala Phe Ser  
 225                      230

<210> 1069  
 <211> 1364  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1341)  
 <223> FRXA01084

<400> 1069  
 tcc ttt ctg gat acc aag cgc gag aac gcc gat gag aag atc cgc atc    48  
 Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile  
   1                      5                      10                      15  
 aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg    96  
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu  
                     20                      25                      30  
 gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag    144  
 Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu  
                     35                      40                      45  
 cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac    192  
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr

50	55	60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala 65 70 75 80			240
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr 85 90 95			288
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu 100 105 110			336
ggg cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser 115 120 125			384
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu 130 135 140			432
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp 145 150 155 160			480
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr 165 170 175			528
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys 180 185 190			576
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His 195 200 205			624
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu 210 215 220			672
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg 225 230 235 240			720
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe 245 250 255			768
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala 260 265 270			816
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys 275 280 285			864
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala 290 295 300			912



gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960  
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac  
 1008  
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc  
 1056  
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc  
 1104  
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe  
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct  
 1152  
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala  
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc  
 1200  
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe  
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca  
 1248  
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala  
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt  
 1296  
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val  
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg  
 1341  
 Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu  
 435 440 445

taaaagcact taaaaatatc ccc  
 1364

<210> 1070

<211> 447

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1070

Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile  
 1 5 10 15

Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu  
 20 25 30

Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu  
                   35                                  40                                  45  
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr  
                   50                                  55                                  60  
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala  
   65                                  70                                  75                                  80  
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr  
                                   85                                  90                                  95  
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu  
                                   100                                  105                                  110  
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser  
                   115                                  120                                  125  
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu  
                   130                                  135                                  140  
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp  
   145                                  150                                  155                                  160  
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr  
                                   165                                  170                                  175  
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys  
                                   180                                  185                                  190  
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His  
                   195                                  200                                  205  
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu  
                   210                                  215                                  220  
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg  
   225                                  230                                  235                                  240  
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe  
                                   245                                  250                                  255  
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala  
                                   260                                  265                                  270  
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys  
                   275                                  280                                  285  
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala  
                   290                                  295                                  300  
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
   305                                  310                                  315                                  320  
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
                                   325                                  330                                  335  
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
                                   340                                  345                                  350  
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe

355	360	365	
Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala			
370	375	380	
Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe			
385	390	395	400
Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala			
	405	410	415
Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val			
	420	425	430
Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu			
435	440	445	

<210> 1071  
 <211> 1125  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1102)  
 <223> RXN01920

<400> 1071  
 cttctgaagg gcttcggttg gggtaagctg gcgatctgaa atcgcgctgc attgtggcgt 60  
 cgaaaagcaa aaaaatttgt agaagggaag agcgcaccta atg gct gct gat tct 115  
 Met Ala Ala Asp Ser  
 1 5  
 gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta 163  
 Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val  
 10 15 20  
 aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc 211  
 Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val  
 25 30 35  
 tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta 259  
 Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val  
 40 45 50  
 tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc 307  
 Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala  
 55 60 65  
 gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag 355  
 Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln  
 70 75 80 85  
 ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac 403  
 Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His  
 90 95 100  
 gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca 451  
 Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala

105	110	115	
aag agt tac tcc aac atc ttc atg act ctg gcc tcc acc gcg gaa atc			499
Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala Ser Thr Ala Glu Ile			
120	125	130	
aac gat gcg ttc cgt tgg tct gag gaa aat gaa aac ctg cag cgc aag			547
Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu Asn Leu Gln Arg Lys			
135	140	145	
gca aag atc atc ctg tct tac tat gag ggc gat gat cca cta aag cgc			595
Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp Asp Pro Leu Lys Arg			
150	155	160	165
aag atc gcc tcc gtg atc ctg gag tcc ttc ctg ttc tac tcc ggc ttc			643
Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu Phe Tyr Ser Gly Phe			
170	175	180	
tac ctc cca atg tat tgg tcc agc cac tcc aag ctg gcc aac acc gcc			691
Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys Leu Ala Asn Thr Ala			
185	190	195	
gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac tac			739
Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr Tyr			
200	205	210	
att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag cgt			787
Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu Arg			
215	220	225	
cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt tac			835
Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu Tyr			
230	235	240	245
gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga tgg			883
Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly Trp			
250	255	260	
acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc ctc			931
Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala Leu			
265	270	275	
aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag gtg			979
Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys Val			
280	285	290	
tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac cac			1027
Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn His			
295	300	305	
gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca gaa			1075
Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala Glu			
310	315	320	325
aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag			1122
Asn Thr Glu Asp Asp Asp Trp Asp Phe			
330			

cgc  
1125

<210> 1072  
<211> 334  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 1072  
Met Ala Ala Asp Ser Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu  
1 5 10 15  
His Val Ala Pro Val Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser  
20 25 30  
Lys Asp Leu Glu Val Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro  
35 40 45  
Glu Lys Val Pro Val Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn  
50 55 60  
Glu Val Glu Lys Ala Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu  
65 70 75 80  
Leu Asp Thr Ile Gln Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp  
85 90 95  
Ala Asp Ser Leu His Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met  
100 105 110  
Glu Ser Val His Ala Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala  
115 120 125  
Ser Thr Ala Glu Ile Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu  
130 135 140  
Asn Leu Gln Arg Lys Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp  
145 150 155 160  
Asp Pro Leu Lys Arg Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu  
165 170 175  
Phe Tyr Ser Gly Phe Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys  
180 185 190  
Leu Ala Asn Thr Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala  
195 200 205  
Val His Gly Tyr Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys  
210 215 220  
Glu Thr Pro Glu Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu  
225 230 235 240  
Leu Tyr Asp Leu Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr  
245 250 255  
Asp Asp Leu Gly Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn  
260 265 270

Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala  
 275 280 285  
 Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn  
 290 295 300  
 Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val  
 305 310 315 320  
 Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 325 330

<210> 1073  
 <211> 437  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(414)  
 <223> FRXA01920

<400> 1073  
 gcc gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac 48  
 Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr  
 1 5 10 15  
 tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag 96  
 Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu  
 20 25 30  
 cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt 144  
 Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu  
 35 40 45  
 tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga 192  
 Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly  
 50 55 60  
 tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc 240  
 Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala  
 65 70 75 80  
 ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag 288  
 Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys  
 85 90 95  
 gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac 336  
 Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn  
 100 105 110  
 cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca 384  
 His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala  
 115 120 125  
 gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 434  
 Glu Asn Thr Glu Asp Asp Trp Asp Phe  
 130 135  
 cgc 437

&lt;210&gt; 1074

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1074

Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr  
 1 5 10 15

Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu  
 20 25 30

Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu  
 35 40 45

Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly  
 50 55 60

Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala  
 65 70 75 80

Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys  
 85 90 95

Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn  
 100 105 110

His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala  
 115 120 125

Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 130 135

&lt;210&gt; 1075

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(544)

&lt;223&gt; RXA01080

&lt;400&gt; 1075

ttcagttcctt cccttcaacg cccttgaagg gggaaactga taccagcaag cacactaggc 60

ttgcgcacaa acggtatttta gaagggaagt gagttcgagg atg cta atc gtg tat 115  
 Met Leu Ile Val Tyr  
 1 5

ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163  
 Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp  
 10 15 20

tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211  
 Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys  
 25 30 35

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atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259
Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val
      40                      45                      50

tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307
Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg
      55                      60                      65

ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355
Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala
      70                      75                      80                      85

ggg gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403
Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile
      90                      95                      100

att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451
Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met
      105                      110                      115

ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499
Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn
      120                      125                      130

gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544
Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg
      135                      140                      145

taaaccttaa aacttaatca atc 567

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&lt;210&gt; 1076

&lt;211&gt; 148

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1076

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Met Leu Ile Val Tyr Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe
  1                      5                      10                      15

Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val
      20                      25                      30

Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr
      35                      40                      45

Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro
      50                      55                      60

Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile
      65                      70                      75                      80

Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly
      85                      90                      95

Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr
      100                      105                      110

Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly
      115                      120                      125

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Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro  
 130 135 140

Val Thr Ser Arg  
 145

<210> 1077

<211> 650

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

ttc ggc gac atg gac ttc aag gtt gcc ggc acc gca gac ttc atc acc	48
Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr	
1 5 10 15	
gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc	96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu	
20 25 30	
tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac	144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn	
35 40 45	
acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct	192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala	
50 55 60	
cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg	240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu	
65 70 75 80	
atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc	288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly	
85 90 95	
gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct	336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala	
100 105 110	
gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg	384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala	
115 120 125	
aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc	432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val	
130 135 140	
aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac	480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp	
145 150 155 160	
ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag	528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys	
165 170 175	

gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576  
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                  185                  190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624  
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
                   195                  200                  205

gac taattagttc tggctagatc ggg 650  
 Asp

<210> 1078

<211> 209

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1078

Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr  
   1                  5                  10                  15

Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu  
                   20                  25                  30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn  
                   35                  40                  45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala  
                   50                  55                  60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu  
                   65                  70                  75                  80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly  
                   85                  90                  95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala  
                   100                  105                  110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala  
                   115                  120                  125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val  
                   130                  135                  140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp  
                   145                  150                  155                  160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys  
                   165                  170                  175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                  185                  190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
                   195                  200                  205

Asp

&lt;210&gt; 1079

&lt;211&gt; 630

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(630)

&lt;223&gt; RXA01416

&lt;400&gt; 1079

gct ggc gct tcc gaa aac gtt gtc aac cgc gtc aag gac ggt gca cca	48
Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro	
1 5 10 15	
gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca	96
Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro	
20 25 30	
ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt	144
Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val	
35 40 45	
gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag	192
Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu	
50 55 60	
gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg	240
Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu	
65 70 75 80	
ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac	288
Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr	
85 90 95	
atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac	336
Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr	
100 105 110	
agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct	384
Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala	
115 120 125	
gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc	432
Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg	
130 135 140	
atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt	480
Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val	
145 150 155 160	
gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag	528
Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu	
165 170 175	
acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag	576
Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln	
180 185 190	

caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624  
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
           195                          200                          205

tac aac 630  
 Tyr Asn  
       210

<210> 1080

<211> 210

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1080

Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro  
       1                          5                          10                          15

Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro  
           20                          25                          30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val  
           35                          40                          45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu  
       50                          55                          60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu  
       65                          70                          75                          80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr  
           85                          90                          95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr  
           100                          105                          110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala  
       115                          120                          125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg  
       130                          135                          140

Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val  
       145                          150                          155                          160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu  
           165                          170                          175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln  
           180                          185                          190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
       195                          200                          205

Tyr Asn  
       210

<210> 1081

<211> 757

<212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(757)

&lt;223&gt; RXA01486

&lt;400&gt; 1081

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agagaactgg taagggtttt accgttctag accgcagaaa tcttcgcggc gacaccgatg 60
atcgccgagc agaactaaac atgaggagac ctactcgcac atg agc gat gta aag 115
Met Ser Asp Val Lys
1 5

gac ttc gaa gac acc gaa ttt ggc ctg atc gag gcc gtc gca acc atc 163
Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu Ala Val Ala Thr Ile
10 15 20

gac aac ggt gac ttc gga acc cgc acc atc cgt ttt gaa acc ggc caa 211
Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg Phe Glu Thr Gly Gln
25 30 35

ctt gcc cgc cag gca gat ggt gca gtg acc acc tac ctc gac gat gac 259
Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr Tyr Leu Asp Asp Asp
40 45 50

acg atg ctg ctg gca acc acc acc gca tcc aac cag cca cgc gag ggc 307
Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn Gln Pro Arg Glu Gly
55 60 65

ttt gac ttc ttc cca ctg acc gtg gac gtt gaa gag cgt atg tac gca 355
Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu Glu Arg Met Tyr Ala
70 75 80 85

gct ggt cgc atc cct ggc tct ttc ttc cgt cgg gag ggt cgc cca tcc 403
Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg Glu Gly Arg Pro Ser
90 95 100

acc gaa gct atc ctg gct tgc cgt ctc atc gac cgc cca ctg cgc cca 451
Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp Arg Pro Leu Arg Pro
105 110 115

acc ttt gtt aag ggc ctg cgc aat gag gtt cag atc gtt gtc acc gtc 499
Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln Ile Val Val Thr Val
120 125 130

atg tcc atg aac cct gag gat tac tac gat gtc gta gca atc aac gga 547
Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val Val Ala Ile Asn Gly
135 140 145

gct tcc gca gca acc cgc atc tcc gga ctt cct gtc tcc ggc gct gtc 595
Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro Val Ser Gly Ala Val
150 155 160 165

ggt ggc gtt cgc atg gca ctg gtt ggt gat gaa aag cac cca gaa ggc 643
Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu Lys His Pro Glu Gly
170 175 180

caa tgg gtt gca ttc cca acc cac gct caa cat gag cag tcc gta ttt 691
Gln Trp Val Ala Phe Pro Thr His Ala Gln His Glu Gln Ser Val Phe
185 190 195

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gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739  
 Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys  
           200                          205                          210

acc ttc tcc gac gtc gca 757  
 Thr Phe Ser Asp Val Ala  
           215

<210> 1082

<211> 219

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1082

Met Ser Asp Val Lys Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu  
       1                          5                          10                          15

Ala Val Ala Thr Ile Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg  
           20                          25                          30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr  
           35                          40                          45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn  
           50                          55                          60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu  
       65                          70                          75                          80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg  
                           85                          90                          95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp  
           100                          105                          110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln  
           115                          120                          125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val  
       130                          135                          140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro  
       145                          150                          155                          160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu  
           165                          170                          175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His  
           180                          185                          190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg  
           195                          200                          205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala  
       210                          215

<210> 1083

<211> 651

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(628)

&lt;223&gt; RXA01678

&lt;400&gt; 1083

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cggttatatc tctgcaactg cagctcaccg cggtgcagca atg ctg aaa tgt gca 115
                               Met Leu Lys Cys Ala
                               1           5

gtc gat gaa gcc gct ggc gga cgc gcc caa gct ttc gta tcc tca ggc 163
Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala Phe Val Ser Ser Gly
          10           15           20

gat aac att ggt ggc agc ccg ttc caa tcc tcc att ctt ggt gat gaa 211
Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser Ile Leu Gly Asp Glu
          25           30           35

ccc acc ttg gaa gca ctc aac caa atg ggt ctt gat tac tca gca gtg 259
Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu Asp Tyr Ser Ala Val
          40           45           50

ggc aac cac gaa ttt gat aaa ggc tac gca gac tta agc agt cga gtc 307
Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp Leu Ser Ser Arg Val
          55           60           65

gct gac ctt gct gat ttt gat tat ctc ggc gca aac gtt gag ggc gaa 355
Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala Asn Val Glu Gly Glu
          70           75           80           85

aac cca gat ctt gca cca tat gga att tct cac ctt gat ggt gtg aag 403
Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His Leu Asp Gly Val Lys
          90           95           100

gtt gct ttc gta ggc acc gta tcc caa gaa act ccg atg ttg gtc aat 451
Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr Pro Met Leu Val Asn
          105           110           115

tct gaa ggc att gag gga atc acg ttt act gac cca ctt gaa gca acc 499
Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp Pro Leu Glu Ala Thr
          120           125           130

aac cgt gta gct gat gaa ctc gtg gga agt ggc gca gca gat gtt gtc 547
Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly Ala Ala Asp Val Val
          135           140           145

gtt gcg ctt tac cac gaa ggc att acc ggc acc gaa gca tgg tca gaa 595
Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr Glu Ala Trp Ser Glu
          150           155           160           165

aat atc gac gtt gtt ttc gca ggt cac acc cac taagttcgtg atctaggaac 648
Asn Ile Asp Val Val Phe Ala Gly His Thr His
          170           175

cga 651

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<210> 1084
<211> 176
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1084															
Met	Leu	Lys	Cys	Ala	Val	Asp	Glu	Ala	Ala	Gly	Gly	Arg	Ala	Gln	Ala
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Phe	Val	Ser	Ser	Gly	Asp	Asn	Ile	Gly	Gly	Ser	Pro	Phe	Gln	Ser	Ser
			20					25					30		
Ile	Leu	Gly	Asp	Glu	Pro	Thr	Leu	Glu	Ala	Leu	Asn	Gln	Met	Gly	Leu
		35					40					45			
Asp	Tyr	Ser	Ala	Val	Gly	Asn	His	Glu	Phe	Asp	Lys	Gly	Tyr	Ala	Asp
	50					55					60				
Leu	Ser	Ser	Arg	Val	Ala	Asp	Leu	Ala	Asp	Phe	Asp	Tyr	Leu	Gly	Ala
65					70					75					80
Asn	Val	Glu	Gly	Glu	Asn	Pro	Asp	Leu	Ala	Pro	Tyr	Gly	Ile	Ser	His
				85					90					95	
Leu	Asp	Gly	Val	Lys	Val	Ala	Phe	Val	Gly	Thr	Val	Ser	Gln	Glu	Thr
			100					105					110		
Pro	Met	Leu	Val	Asn	Ser	Glu	Gly	Ile	Glu	Gly	Ile	Thr	Phe	Thr	Asp
		115					120					125			
Pro	Leu	Glu	Ala	Thr	Asn	Arg	Val	Ala	Asp	Glu	Leu	Val	Gly	Ser	Gly
	130					135					140				
Ala	Ala	Asp	Val	Val	Val	Ala	Leu	Tyr	His	Glu	Gly	Ile	Thr	Gly	Thr
145					150					155					160
Glu	Ala	Trp	Ser	Glu	Asn	Ile	Asp	Val	Val	Phe	Ala	Gly	His	Thr	His
				165					170					175	

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<210> 1085
<211> 1359
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1336)
<223> RXA01679
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<400> 1085
cattaccggc accgaagcat ggtcagaaaa tatcgacgtt gttttcgcag gtcacacca 60

ctaagtctgt gatctaggaa cgcacaacgg tccactaatc atg cag tct gga aac 115
                                     Met Gln Ser Gly Asn
                                     1           5

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tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc	163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
10 15 20	
ggt gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tcc gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
200 205 210	
gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly  
 250 255 260  
 caa gcc cag att tcc atc acc cca tcc ggt gag ttc aat gcg ggt gaa 931  
 Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu  
 265 270 275  
 acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979  
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr  
 280 285 290  
 gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca  
 1027  
 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro  
 295 300 305  
 att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg  
 1075  
 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala  
 310 315 320 325  
 aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc  
 1123  
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu  
 330 335 340  
 gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att  
 1171  
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile  
 345 350 355  
 gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta  
 1219  
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu  
 360 365 370  
 gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta  
 1267  
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu  
 375 380 385  
 gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag  
 1315  
 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln  
 390 395 400 405  
 atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat  
 1359  
 Ile Gln Gln Gln Ile Phe Ala  
 410

&lt;210&gt; 1086

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1086

Met Gln Ser Gly Asn Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser  
 1 5 10 15

Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu  
                     20                    25                    30  
 Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala  
                     35                    40                    45  
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu  
                     50                    55                    60  
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly  
                     65                    70                    75                    80  
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met  
                     85                    90                    95  
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr  
                     100                    105                    110  
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe  
                     115                    120                    125  
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser  
                     130                    135                    140  
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala  
                     145                    150                    155                    160  
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu  
                     165                    170                    175  
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile  
                     180                    185                    190  
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro  
                     195                    200                    205  
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn  
                     210                    215                    220  
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly  
                     225                    230                    235                    240  
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val  
                     245                    250                    255  
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu  
                     260                    265                    270  
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr  
                     275                    280                    285  
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu  
                     290                    295                    300  
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly  
                     305                    310                    315                    320  
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser  
                     325                    330                    335  
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser

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340                      345                      350
Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala
355                      360                      365

Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile
370                      375                      380

Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro
385                      390                      395                      400

Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala
405                      410

<210> 1087
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXN01488

<400> 1087
ccagcgctta aggccggtca ccggccatca agcttggtcac atcggggtgcc ttatgatggt 60

gcccgcacctt aaaaataaaa acctgaaagg ttaaaaacgc atg agc aaa aaa gcc 115
Met Ser Lys Lys Ala
1 5

atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac 163
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr
10 15 20

gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac 211
Ala Leu Gly Ser Pro Glu Leu Glu Ile Gly Val Thr Thr Thr Tyr
25 30 35

ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt 259
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu
40 45 50

gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac 307
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His
55 60 65

gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att 355
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile
70 75 80 85

cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca 403
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser
90 95 100

aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc 451
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr
105 110 115

cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg 499

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His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu  
 120 125 130  
 tct gcg gca atc gca aag gat cca agc ttt gct tcc aag gct cac gtg 547  
 Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val  
 135 140 145  
 gtc atc atg ggt ggc gcc ttg act gtc cca ggc aac gtc agc aca tgg 595  
 Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp  
 150 155 160 165  
 gca gaa gca aac atc aac cag gac cca gat gca gca aac gat ctg ttc 643  
 Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe  
 170 175 180  
 cgt tcc ggt gca gat gtc acc atg atc ggt ctt gat gtc acc ctg cag 691  
 Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln  
 185 190 195  
 acc ctt ctt acc aag aag cac act gcg cag tgg cgc gaa ctg ggc act 739  
 Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr  
 200 205 210  
 cca gct gct atc gca ctg gcc gac atg act gat tac tac atc aag gca 787  
 Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala  
 215 220 225  
 tat gag acc acc gca cca cac ctg ggc ggt tgc ggc ctg cac gac cca 835  
 Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro  
 230 235 240 245  
 ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act ttg ctc ccc 883  
 Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro  
 250 255 260  
 atc aac ctc aag gta gac att gag ggc gag acc cgt gga cgc acc att 931  
 Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile  
 265 270 275  
 ggc gat gaa gtc cgc ctc aac gat cca gtg cgc acc tcc cgc gca gct 979  
 Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala  
 280 285 290  
 gtc gcc gta gac gtg gat cgt ttc ctt tct gaa ttc atg acc cgc atc  
 1027  
 Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile  
 295 300 305  
 ggc cga gtc gca gca cag cag taaaagcagc tctggtgaag gtt  
 1071  
 Gly Arg Val Ala Ala Gln Gln  
 310 315

&lt;210&gt; 1088

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1088

Met Ser Lys Lys Ala Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala

1	5	10	15
Leu Ala Leu	Ala Tyr	Ala Leu Gly Ser	Pro Glu Leu Glu Leu Ile Gly
	20	25	30
Val Thr Thr	Thr Tyr Gly Asn	Val Leu Leu Glu Thr	Gly Ala Val Asn
	35	40	45
Asp Leu Ala	Leu Leu Asp	Leu Phe Gly Ala	Pro Glu Val Pro Val Tyr
	50	55	60
Leu Gly Glu	Pro His Ala Gln	Thr Lys Asp Gly	Phe Glu Val Leu Glu
	65	70	75
Ile Ser Ala	Phe Ile His Gly	Gln Asn Gly Ile	Gly Glu Val Glu Leu
	85	90	95
Pro Ala Ser	Glu Ser Lys Ala	Leu Pro Gly Ala	Val Asp Phe Leu Ile
	100	105	110
Asp Ser Val	Asn Thr His Gly	Asp Leu Val Ile	Ile Ala Thr Gly
	115	120	125
Pro Met Thr	Asn Leu Ser Ala	Ala Ile Ala Lys	Asp Pro Ser Phe Ala
	130	135	140
Ser Lys Ala	His Val Val Ile	Met Gly Gly Ala	Leu Thr Val Pro Gly
	145	150	155
Asn Val Ser	Thr Trp Ala Glu	Ala Asn Ile Asn	Gln Asp Pro Asp Ala
	165	170	175
Ala Asn Asp	Leu Phe Arg Ser	Gly Ala Asp Val	Thr Met Ile Gly Leu
	180	185	190
Asp Val Thr	Leu Gln Thr Leu	Leu Thr Lys Lys	His Thr Ala Gln Trp
	195	200	205
Arg Glu Leu	Gly Thr Pro Ala	Ala Ile Ala Leu	Ala Asp Met Thr Asp
	210	215	220
Tyr Tyr Ile	Lys Ala Tyr Glu	Thr Thr Ala Pro	His Leu Gly Gly Cys
	225	230	235
Gly Leu His	Asp Pro Leu Ala	Val Gly Val Ala	Val Asp Pro Ser Leu
	245	250	255
Val Thr Leu	Leu Pro Ile Asn	Leu Lys Val Asp	Ile Glu Gly Glu Thr
	260	265	270
Arg Gly Arg	Thr Ile Gly Asp	Glu Val Arg Leu	Asn Asp Pro Val Arg
	275	280	285
Thr Ser Arg	Ala Ala Val Ala	Val Asp Val Asp	Arg Phe Leu Ser Glu
	290	295	300
Phe Met Thr	Arg Ile Gly Arg	Val Ala Ala Gln	Gln
	305	310	315

&lt;210&gt; 1089



<210> 1091  
 <211> 498  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(475)  
 <223> RXC00560

<400> 1091  
 aaggacgact tctggggagc ggtgtggatt ctcacgggga ttctcatgcg gattatcaga 60  
 catatggaca ctttaacggt tcgtactagg ctgatgcttc atg agg att gat ccg 115  
 Met Arg Ile Asp Pro  
 1 5  
 ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163  
 Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly  
 10 15 20  
 gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211  
 Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr  
 25 30 35  
 cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259  
 Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val  
 40 45 50  
 gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307  
 Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro  
 55 60 65  
 aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag 355  
 Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys  
 70 75 80 85  
 acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt 403  
 Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe  
 90 95 100  
 gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg 451  
 Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala  
 105 110 115  
 gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt 498  
 Asp Trp Leu Pro Val Val Lys Leu  
 120 125

<210> 1092  
 <211> 125  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1092  
 Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys  
 1 5 10 15



Asp	Trp	Ile	Glu	Gly	Glu	Gly	Asp	Val	Lys	Lys	Pro	Gly	Arg	Ala	Ala	
			20				25						30			
Leu	Ala	Ala	Ala	Thr	Arg	Leu	Ser	Val	Arg	Leu	Leu	Ala	Gln	His	Ala	
			35				40						45			
Pro	Gly	Asn	Ser	Val	Glu	Val	Arg	Val	Pro	Pro	Phe	Val	Ala	Val	Gln	
			50				55						60			
Cys	Ile	Glu	Gly	Pro	Lys	His	Thr	Arg	Gly	Thr	Pro	Pro	Asn	Val	Val	
			65				70						80			
Glu	Thr	Asp	Ala	Lys	Thr	Trp	Leu	Arg	Leu	Ala	Pro	Gly	Gln	Thr	Thr	
			85						90						95	
Phe	Asp	Ala	Glu	Phe	Glu	Ser	Gly	Lys	Ile	Ser	Ala	Ser	Gly	Thr	Arg	
			100						105						110	
Ala	Lys	Glu	Ile	Ala	Asp	Trp	Leu	Pro	Val	Val	Lys	Leu				
			115						120			125				

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<210> 1093
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1282)  
<223> RXC01088
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<400> 1093																								
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gtga	acc	cgaa	tttt	tt	ta	act	gatt	t	ga	aga	agc	gaga	ata	atg	gga	ctg	tgg	atc				115		
														Met	Gly	Leu	Trp	Ile		1			5	
gat	gca	acc	gct	ggc	gtt	gca	ggg	gat	atg	ttg	ctg	gga	gca	ctc	att							163		
Asp	Ala	Thr	Ala	Gly	Val	Ala	Gly	Asp	Met	Leu	Leu	Gly	Ala	Leu	Ile									
				10					15					20										
gat	gca	ggt	gca	gaa	cta	gaa	aaa	atc	caa	cag	gtt	gtg	gaa	gca	gtc							211		
Asp	Ala	Gly	Ala	Glu	Leu	Glu	Lys	Ile	Gln	Gln	Val	Val	Glu	Ala	Val									
				25					30					35										
atc	ccc	ggt	gac	gtg	ctc	ttg	cgc	acc	gaa	gag	gta	gtg	cgc	caa	ggc							259		
Ile	Pro	Gly	Asp	Val	Leu	Leu	Arg	Thr	Glu	Glu	Val	Val	Arg	Gln	Gly									
				40					45					50										
caa	cga	ggc	atc	aag	ctg	cat	gtg	gac	gca	caa	cat	gaa	cac	cat	cat							307		
Gln	Arg	Gly	Ile	Lys	Leu	His	Val	Asp	Ala	Gln	His	Glu	His	His	His									
				55					60					65										
cac	cgc	cac	tta	agc	acc	att	aaa	gaa	ctg	ctt	gtc	aat	gct	gac	atc							355		
His	Arg	His	Leu	Ser	Thr	Ile	Lys	Glu	Leu	Leu	Val	Asn	Ala	Asp	Ile									
				70					75					80					85					
cct	gaa	caa	acc	aag	cag	gat	gcc	tta	ggc	gtt	ttt	gaa	ctc	atc	gct							403		

Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala  
90 95 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451  
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe  
105 110 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499  
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys  
120 125 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547  
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile  
135 140 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595  
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val  
150 155 160 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc 643  
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr  
170 175 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca 691  
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro  
185 190 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc 739  
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe  
200 205 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat 787  
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp  
215 220 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct 835  
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser  
230 235 240 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt 883  
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val  
250 255 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt 931  
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe  
265 270 275

gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag 979  
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys  
280 285 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg  
1027  
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val  
295 300 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc  
1075  
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile  
310 315 320 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa  
1123

Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln  
330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat  
1171

Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp  
345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca  
1219

Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala  
360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg  
1267

Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro  
375 380 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct  
1305

Gln Gly Thr Thr Glu  
390

<210> 1094

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1094

Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu  
1 5 10 15

Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln  
20 25 30

Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu  
35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln  
50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu  
65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val  
85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro  
100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp  
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile  
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His  
145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly  
 165 170 175  
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly  
 180 185 190  
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr  
 195 200 205  
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly  
 210 215 220  
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile  
 225 230 235 240  
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln  
 245 250 255  
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val  
 260 265 270  
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro  
 275 280 285  
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val  
 290 295 300  
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr  
 305 310 315 320  
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp  
 325 330 335  
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys  
 340 345 350  
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu  
 355 360 365  
 Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val  
 370 375 380  
 Val Ala Arg Ile Pro Gln Gly Thr Thr Glu  
 385 390

&lt;210&gt; 1095

&lt;211&gt; 1419

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

&lt;223&gt; RXC02624

&lt;400&gt; 1095

accgggtcag atccgacgtc gccggccaaa accgcaagca cctgcgcaaa cgccacagaa 60

ggcagctcag caatcaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115

	Val	Leu	Ile	Pro	His	
	1				5	
ggc gtg gcg gtg ctt ttg gtt att att ctc gcc gta gcc tcc cta atg						163
Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala Val Ala Ser Leu Met						
	10			15	20	
ttc acc aat tct tca atg gtg aat ctt tcg gca acg att gca cag ctg						211
Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala Thr Ile Ala Gln Leu						
	25		30		35	
tgg ctt tcc cta aat ctc ggt gcg gtg gac ggc agt ggg gaa gtg atc						259
Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly Ser Gly Glu Val Ile						
	40		45		50	
tca gta ctg ccc acg ctt ccc ggc ttt ata ttc ctc tgg gcc atc gcc						307
Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe Leu Trp Ala Ile Ala						
	55		60		65	
gcg cgc atc cac cgc gca gtc aaa gat cgt gtc agc atc gcc gac tta						355
Ala Arg Ile His Arg Ala Val Lys Asp Arg Val Ser Ile Ala Asp Leu						
	70		75		80	85
ggc gtc ctc gca gca ctc gtc ctc ggc atc ccg ctt gcg ctc acc gcc						403
Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro Leu Ala Leu Thr Ala						
	90		95		100	
atc gca gcg ttc atg ctt ttc gac gcc tcc agc gtc ctc aac gtc gag						451
Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser Val Leu Asn Val Glu						
	105		110		115	
gtc ccg cca atc acg cgc ctc cta cgc gtg atg ttg ttc cac ctc agc						499
Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met Leu Phe His Leu Ser						
	120		125		130	
gcc ctc ttc ctc ggc atg ggg cca cgc ctg tgg cag gcg ttg gcg cgc						547
Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp Gln Ala Leu Ala Arg						
	135		140		145	
cgc tac ggt gct cca gaa tgg ctt atc gac gcc atc acc caa gct ttc						595
Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala Ile Thr Gln Ala Phe						
	150		155		160	165
cgc ttc ctc atc gca ttt gga aca gtc tcc ttg gtt tcc gtg ctc gtg						643
Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu Val Ser Val Leu Val						
	170		175		180	
atg acc gcg atc aac cac agt gca ttc acc gcg acc atg cag ggt tac						691
Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala Thr Met Gln Gly Tyr						
	185		190		195	
gac gac tcc gcc tct gtt gtg gcc ttg atc gtc ctg agc att ctg tat						739
Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser Ile Leu Tyr						
	200		205		210	
ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc ggc tca ccc						787
Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile Gly Ser Pro						
	215		220		225	
ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg cat tcc gtt						835
Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val His Ser Val						

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu				
	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp				
	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala				
	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
1027				
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly				
	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
1075				
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val				
	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
1123				
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly				
	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
1171				
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val				
	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
1219				
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu				
	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
1267				
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly				
	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
1315				
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro				
	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
1363				
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu				
	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
1416				
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg				
	425	430		
ctg				
1419				

&lt;210&gt; 1096

&lt;211&gt; 432

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala  
 1 5 10 15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala  
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly  
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe  
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val  
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro  
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser  
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met  
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp  
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala  
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu  
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala  
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val  
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn  
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe  
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu  
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala  
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val  
 275 280 285

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala  
 290 295 300  
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn  
 305 310 315 320  
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly  
 325 330 335  
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys  
 340 345 350  
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu  
 355 360 365  
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu  
 370 375 380  
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp  
 385 390 395 400  
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr  
 405 410 415  
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg  
 420 425 430

&lt;210&gt; 1097

&lt;211&gt; 603

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; RXC02665

&lt;400&gt; 1097

caaggcgacc caatggcggt taaagtaaca acccccattg atatgatgct ggcacaacgc 60

 atcaccgacg aagccgaacc cacaatatatt gaggtaccag gtg act aac cca atc 115  
 Val Thr Asn Pro Ile  
 1 5

 atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163  
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly  
 10 15 20

 aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211  
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys  
 25 30 35

 gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259  
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala  
 40 45 50



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ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307
Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
    55                60                65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355
Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
    70                75                80                85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403
Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
                90                95                100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451
Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu
                105                110                115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499
Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
                120                125                130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547
Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
                135                140                145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600
Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
    150                155                160

ggc 603

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<210> 1098  
 <211> 160  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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<400> 1098
Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
  1                5                10                15

Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
    20                25                30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
    35                40                45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
    50                55                60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
    65                70                75                80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
    85                90                95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
    100                105                110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
    115                120                125

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Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly  
 130 135 140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
 145 150 155 160

<210> 1099

<211> 1689

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1666)

<223> RXC02770

<400> 1099

tcgccggggc aaaaaccgta taattacagt cctattacga ttcggggaaa ggctgggtac 60

ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg 115  
 Met Leu Val Ala Ala  
 1 5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163  
 Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His  
 10 15 20

caa aca agc ctt ttc ggc tac gca gtt aac tct tgc ctg gct aca acc 211  
 Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr  
 25 30 35

aac gcg gcg tgc ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259  
 Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala  
 40 45 50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307  
 Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met  
 55 60 65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355  
 Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn  
 70 75 80 85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403  
 Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly  
 90 95 100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451  
 Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln  
 105 110 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tgc cag att gag 499  
 Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu  
 120 125 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547  
 Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg			595
Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu			
150	155	160	165
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag			643
Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu			
	170	175	180
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct			691
Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro			
	185	190	195
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag			739
Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu			
	200	205	210
ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc			787
Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe			
	215	220	225
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg			835
Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala			
	230	235	240
ggt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc			883
Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala			
	250	255	260
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag			931
Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu			
	265	270	275
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att			979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile			
	280	285	290
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc			
1027			
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala			
	295	300	305
ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt			
1075			
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val			
	310	315	320
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat			
1123			
Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp			
	330	335	340
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg			
1171			
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val			
	345	350	355
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat			
1219			
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			

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360          365          370
gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga
1267
Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly
375          380          385

ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt
1315
Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys
390          395          400          405

gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt
1363
Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser
410          415          420

ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag
1411
Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln
425          430          435

tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat
1459
Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His
440          445          450

cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg
1507
Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr
455          460          465

agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta
1555
Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu
470          475          480          485

gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt
1603
Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val
490          495          500

gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg
1651
Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp
505          510          515

tcc aga agt gag gaa taagtagtga gcgaacaagc tct
1689
Ser Arg Ser Glu Glu
520

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&lt;210&gt; 1100

&lt;211&gt; 522

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1100

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Met Leu Val Ala Ala Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro
1          5          10          15

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Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser  
 20 25 30  
 Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp  
 35 40 45  
 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly  
 50 55 60  
 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val  
 65 70 75 80  
 Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala  
 85 90 95  
 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser  
 100 105 110  
 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu  
 115 120 125  
 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala  
 130 135 140  
 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe  
 145 150 155 160  
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly  
 165 170 175  
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu  
 180 185 190  
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser  
 195 200 205  
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp  
 210 215 220  
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr  
 225 230 235 240  
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly  
 245 250 255  
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His  
 260 265 270  
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu  
 275 280 285  
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu  
 290 295 300  
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala  
 305 310 315 320  
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser  
 325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His  
 340 345 350  
 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met  
 355 360 365  
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg  
 370 375 380  
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala  
 385 390 395 400  
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser  
 405 410 415  
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu  
 420 425 430  
 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg  
 435 440 445  
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr  
 450 455 460  
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val  
 465 470 475 480  
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg  
 485 490 495  
 Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp  
 500 505 510  
 Asn Met Asp Arg Trp Ser Arg Ser Glu Glu  
 515 520

<210> 1101  
 <211> 408  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(385)  
 <223> RXC02238

<400> 1101  
 ggcgccttagc caaaacatag agcggtaggg tatgcttata cgattgagca acctttcccg 60  
 ctcttaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115  
 Val Thr Asn Val Ser 5  
 1  
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 20  
 10 15  
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr 35  
 25 30

```

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
      40                      45                      50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
      55                      60                      65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
      70                      75                      80                      85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      90                      95

cac 408

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<210> 1102
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

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<400> 1102
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
  1                      5                      10                      15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
      20                      25                      30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
      35                      40                      45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
      50                      55                      60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
      65                      70                      75                      80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      85                      90                      95

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<210> 1103
<211> 1298
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(1275)
<223> RXC01946

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atc cgc aag tac tcc agg ctc gag gaa caa ttc cag tcg ctc ggc ggc 48
Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly
  1                      5                      10                      15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96

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Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu		
			20					25					30				
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144	
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln		
		35				40					45						
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192	
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly		
	50					55					60						
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240	
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His		
	65				70					75					80		
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288	
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His		
				85				90						95			
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336	
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala		
			100					105						110			
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384	
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp		
		115					120					125					
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432	
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp		
	130					135					140						
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480	
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly		
	145				150					155					160		
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528	
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala		
			165					170						175			
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576	
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn		
			180					185						190			
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624	
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro		
		195					200					205					
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672	
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr		
	210					215					220						
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720	
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile		
	225				230					235					240		
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggc	gca	ggc	aaa	768	
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys		
				245				250						255			
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggc	gtg	gaa	cgc	acc	gac	ggc	gaa	816	
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu		



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                260                265                270
ggc ggc atc gtc acc gga tac ggc ctc aaa atc ggc tac ttc gcc cag      864
Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
                275                280                285

gaa cac gac acc atc gac ccc gac aaa tcc gtc tgg caa aac acc atc      912
Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
                290                295                300

gaa gcc tgc gcc gac gcc gac caa caa agc ctc cgc agc ctc ctc gga      960
Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly
305                310                315                320

tcc ttc atg ttc tcc ggc gaa caa ctc gac caa cca gca gga aca ctc
1008
Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
                325                330                335

tcc ggc ggt gaa aaa acc cgc ctc gca ctg gcc acc ctc gtg tcc tcc
1056
Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
                340                345                350

cgc gca aac gtc ctg ctt ctc gac gag ccc acc aac aac ctt gac ccg
1104
Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
                355                360                365

atc tcc cgc gaa cag gtc ctc gac gca ctg cgc acc tac acc ggc gca
1152
Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
                370                375                380

gtc gtc ctg gtt acc cac gac ccg ggt gca gtc aag gcc ctt gag cca
1200
Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
385                390                395                400

gaa cgc gtc atc gtg ctt cct gat ggc acc gag gat ctt tgg aat gat
1248
Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp
                405                410                415

cag tac atg gaa atc gtg gaa ttg gcg taggttctaa ggctgtttat
1295
Gln Tyr Met Glu Ile Val Glu Leu Ala
                420                425

gct
1298

<210> 1104
<211> 425
<212> PRT
<213> Corynebacterium glutamicum

<400> 1104
Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly
  1                5                10                15

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Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu  
                   20                                  25                                  30  
 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln  
                   35                                  40                                  45  
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly  
                   50                                  55                                  60  
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His  
                   65                                  70                                  75                                  80  
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His  
                                   85                                  90                                  95  
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala  
                   100                                  105                                  110  
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp  
                   115                                  120                                  125  
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp  
                   130                                  135                                  140  
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly  
                   145                                  150                                  155                                  160  
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala  
                                   165                                  170                                  175  
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn  
                                   180                                  185                                  190  
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro  
                   195                                  200                                  205  
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr  
                   210                                  215                                  220  
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile  
                   225                                  230                                  235                                  240  
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys  
                                   245                                  250                                  255  
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu  
                   260                                  265                                  270  
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln  
                   275                                  280                                  285  
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile  
                   290                                  295                                  300  
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly  
                   305                                  310                                  315                                  320  
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu  
                                   325                                  330                                  335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser  
 340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro  
 355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala  
 370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro  
 385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp  
 405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala  
 420 425

&lt;210&gt; 1105

&lt;211&gt; 613

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXN03171

&lt;400&gt; 1105

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cggctcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115  
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130  
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145  
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165  
 gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
 170

&lt;210&gt; 1106

&lt;211&gt; 171

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
 1 5 10 15  
 Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
 20 25 30  
 Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
 35 40 45  
 Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
 50 55 60  
 Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
 65 70 75 80  
 Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
 85 90 95  
 Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
 100 105 110  
 Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
 115 120 125  
 Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
 130 135 140  
 Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
 145 150 155 160  
 Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
 165 170

&lt;210&gt; 1107

<211> 613  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> FRXA02857

<400> 1107  
 atactttgtt ggactggaaa agtggccgtt tggttccctc caagcccaaa ttcgcccgcg 60

cggtcttctt ctgggcgga atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tgc atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
 170

```

<400> 1108
Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
  1           5           10           15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
          20           25           30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
          35           40           45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
  50           55           60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
  65           70           75           80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
          85           90           95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
          100          105          110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
          115          120          125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
          130          135          140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
          145          150          155          160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
          165          170

```

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<220>
<221> CDS
<222> (101) .. (424)
<223> RXN00450
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1512

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gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
      25              30              35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
      40              45              50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
      55              60              65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
      70              75              80              85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
      90              95              100

ggt gct cga atc gga cgc atc 424
Gly Ala Arg Ile Gly Arg Ile
      105

```

&lt;210&gt; 1110

&lt;211&gt; 108

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1110

```

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1              5              10              15

```

```

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20              25              30

```

```

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35              40              45

```

```

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50              55              60

```

```

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
      65              70              75              80

```

```

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
      85              90              95

```

```

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
      100              105

```

&lt;210&gt; 1111

&lt;211&gt; 418

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(418)

&lt;223&gt; FRXA00450

&lt;400&gt; 1111

```

tttgcgatga catggatttg gatccttccg aacaattgct gcgcacgcgc gaagaactcg 60

gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115
                                         Val Gly Val Leu Pro
                                         1           5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
                10                15                20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
                25                30                35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
                40                45                50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
                55                60                65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
                70                75                80                85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
                90                95                100

ggg gct cga atc gga
Gly Ala Arg Ile Gly
                105

```

&lt;210&gt; 1112

&lt;211&gt; 106

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1112

```

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
 1           5           10           15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20                25                30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35                40                45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50                55                60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65                70                75                80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85                90                95

```



Ala Gly Ala Leu Val Gly Ala Arg Ile Gly  
 100 105

<210> 1113

<211> 615

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

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tccccaacgc gcaccgaact tagccggatc gcagacttca cctggatgtc caccgcagcc 60
caagcgctac cagcgttgat gcgagggttg agcgcctaac atg act gaa gat gac 115
Met Thr Glu Asp Asp
1 5

tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
10 15 20

cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala
25 30 35

gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
40 45 50

cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
55 60 65

tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
70 75 80 85

atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
90 95 100

gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
105 110 115

gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
120 125 130

ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu
135 140 145

ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu
150 155 160

```

tagcgctggg catgtgactt taa

615

&lt;210&gt; 1114

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1114

Met	Thr	Glu	Asp	Asp	Leu	Asp	Leu	Leu	His	Arg	Thr	Val	Glu	Leu	Ala
1				5					10					15	

Thr	Gln	Ala	Leu	Lys	Gln	Gly	Asn	Ser	Pro	Tyr	Gly	Ser	Leu	Leu	Val
			20					25					30		

Asp	Pro	Phe	Gly	Ala	Val	Val	Phe	Glu	Asp	His	Asn	Arg	Asp	Ala	Asp
		35						40				45			

Gly	Asp	Leu	Thr	Lys	His	Pro	Glu	Phe	Ala	Ile	Ala	Lys	Tyr	Ala	Ile
	50					55					60				

Glu	Asn	Tyr	Ser	Ala	Ser	Glu	Arg	Ala	Ala	Cys	Thr	Val	Tyr	Thr	Ser
65					70					75					80

Thr	Glu	His	Cys	Ala	Met	Cys	Ala	Gly	Ala	His	Ala	Trp	Ala	Gly	Leu
				85						90					95

Gly	Lys	Ile	Tyr	Cys	Ala	Thr	Thr	Gly	Gly	Gln	Thr	Ala	Ala	Trp	Tyr
			100					105					110		

Ala	Lys	Trp	Gly	Ala	Glu	Ser	Gly	Pro	Leu	Asn	Pro	Ile	Ser	Ala	Asp
		115					120					125			

Lys	Ile	Ser	Pro	Asn	Ile	Ser	Ile	Glu	Gly	Pro	Ala	Ser	Arg	Phe	Glu
	130					135					140				

Glu	Val	Leu	Tyr	Glu	Leu	His	Arg	Trp	Phe	Tyr	Leu	Gly	Gln	Ser	Pro
145					150					155					160

Asn Lys Ala Leu

&lt;210&gt; 1115

&lt;211&gt; 1083

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1060)

&lt;223&gt; RXA00717

&lt;400&gt; 1115

aagcatcagc taaagccccg actattaaaa tctcctaaaa taggctagaa ttcacgggat 60

tcaatttcat	acgttttctc	tcaagattaa	ggacacttac	gtg	acc	cca	ccc	gct	115
				Val	Thr	Pro	Pro	Ala	
				1				5	

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10 15 20	
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	
ggg ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120 125 130	
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135 140 145	
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150 155 160 165	
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170 175 180	
ggg cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp	
185 190 195	
ggg gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag	739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
200 205 210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215 220 225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac	835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230 235 240 245	
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc	883

Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile  
 250 255 260  
 gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931  
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu  
 265 270 275  
 ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979  
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val  
 280 285 290  
 cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct  
 1027  
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser  
 295 300 305  
 gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg  
 1080  
 Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 310 315 320  
 cct  
 1083  
 <210> 1116  
 <211> 320  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 1116  
 Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser  
 1 5 10 15  
 Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly  
 20 25 30  
 Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile  
 35 40 45  
 Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp  
 50 55 60  
 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val  
 65 70 75 80  
 Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His  
 85 90 95  
 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile  
 100 105 110  
 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg  
 115 120 125  
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val  
 130 135 140  
 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly  
 145 150 155 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln  
 165 170 175  
 Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu  
 180 185 190  
 Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys  
 195 200 205  
 Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr  
 210 215 220  
 Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly  
 225 230 235 240  
 Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys  
 245 250 255  
 Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg  
 260 265 270  
 Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr  
 275 280 285  
 Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg  
 290 295 300  
 Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 305 310 315 320

&lt;210&gt; 1117

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(955)

&lt;223&gt; RXA01894

&lt;400&gt; 1117

agaatttttt cgaaatgct ggcaccatca acagtgcacat tgtagaaac ttcaaggaga 60

acccatgaat gaaccggagc aacatcacccg gtccatgagg atg ccc aaa ccc aaa 115  
 Met Pro Lys Pro Lys  
 1 5

aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163  
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly  
 10 15 20

ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211  
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp  
 25 30 35

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259  
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

40	45	50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile 55 60 65			307
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met 70 75 80 85			355
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe 90 95 100			403
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg 105 110 115			451
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly 120 125 130			499
agc ttc gct gcg atg ctg tcg ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly 135 140 145			547
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tcg gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val 150 155 160 165			595
ggc ggc tat atc gcg ggt gtg ttc ttt gga tcg cac cca atg gcg ccg Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro 170 175 180			643
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val 185 190 195			691
tta gga tcg gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His 200 205 210			739
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala 215 220 225			787
acg ttg ggt gac ttg gtt gag tcg cag ttc aaa cgc gat ttg ggc atc Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile 230 235 240 245			835
aag gat atg tcg aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg 250 255 260			883
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser 265 270 275			931
gtg atc agc agc tcg tat ccg tcg taaagcttgg gccagcttta agt Val Ile Ser Ser Tyr Pro Ser 280 285			978

&lt;210&gt; 1118

&lt;211&gt; 285

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1118

```

Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile
  1           5           10           15

Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu
      20           25           30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
      35           40           45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
      50           55           60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
      65           70           75           80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
      85           90           95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
      100          105          110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
      115          120          125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
      130          135          140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
      145          150          155          160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
      165          170          175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
      180          185          190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
      195          200          205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
      210          215          220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
      225          230          235          240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
      245          250          255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
      260          265          270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
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 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(856)  
 <223> RXA02536

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 Met Asp Asn Phe Ala  
 1 5  
 ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163  
 Leu Leu Arg Asp Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val  
 10 15 20  
 ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211  
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu  
 25 30 35  
 gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259  
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg  
 40 45 50  
 aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307  
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr  
 55 60 65  
 cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355  
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn  
 70 75 80 85  
 aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403  
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys  
 90 95 100  
 att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451  
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys  
 105 110 115  
 ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499  
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly  
 120 125 130  
 gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547  
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu  
 135 140 145  
 gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595  
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp  
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 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala



				170				175				180					
ctg	gat	tcc	acc	tgc	tg	atc	gta	gcg	tgt	ggg	caa	gcg	cga	ctt	cca	691	
Leu	Asp	Ser	Thr	Cys	Trp	Ile	Val	Ala	Cys	Gly	Gln	Ala	Arg	Leu	Pro		
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gaa	gaa	tta	cgc	gat	gaa	cga	aaa	ggc	cct	acg	ggg	att	gg	cat	tcc	739	
Glu	Glu	Leu	Arg	Asp	Glu	Arg	Lys	Gly	Pro	Thr	Gly	Ile	Gly	His	Ser		
				200				205				210					
atg	gtg	aca	aac	cca	cac	ggt	gaa	gta	att	gct	agc	gcg	gg	tat	gag	787	
Met	Val	Thr	Asn	Pro	His	Gly	Glu	Val	Ile	Ala	Ser	Ala	Gly	Tyr	Glu		
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cca	gaa	atg	ttg	atc	gcg	gat	att	gat	gtc	agc	gg	ttg	gcc	aaa	att	835	
Pro	Glu	Met	Leu	Ile	Ala	Asp	Ile	Asp	Val	Ser	Gly	Leu	Ala	Lys	Ile		
230				235				240				245					
cgg	gag	gca	ttg	cct	gtt	ctt	taaccactgt				ctaaggaatc				act		879
Arg	Glu	Ala	Leu	Pro	Val	Leu											
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<213> Corynebacterium glutamicum
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Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe
          35          40          45
Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val
          50          55          60
Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr
          65          70          75          80
Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His
          85          90          95
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu
          100          105          110
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp
          115          120          125
Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu
          130          135          140
Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro
          145          150          155          160
Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu
          165          170          175

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Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly  
180 185 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr  
195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala  
210 215 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser  
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Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu  
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<210> 1121

<211> 1528

**<212> DNA**

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1528)

<223> RXN01209

<400> 1121

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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
Met Cys Glu Arg Pro  
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
10 15 20

ttg	ggt	ggc	ggg	cca	aaa	aaa	gta	gct	gga	att	gtt	gac	agc	gca	att	211
Leu	Gly	Gly	Gly	Pro	Lys	Lys	Val	Ala	Gly	Ile	Val	Asp	Ser	Ala	Ile	
			25					30					35			

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259  
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val  
40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307  
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala  
55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355  
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu  
70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403  
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln  
90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451  
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu  
105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499  
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly  
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acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595  
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu  
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atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643  
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly  
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ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691  
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 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala  
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787  
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu  
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835  
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn  
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tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883  
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr  
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ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931  
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly  
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
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ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
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 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
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 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
                   345                                  350                                  355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
                   360                                  365                                  370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
                   375                                  380                                  385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
                   390                                  395                                  400                                  405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
                                   410                                  415                                  420

ggc gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
                   425                                  430                                  435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
                   440                                  445                                  450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
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 <213> Corynebacterium glutamicum

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                   20                                  25                                  30  
 Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
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Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
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 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
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 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370	375	380	
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Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr			
	405	410	415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn			
	420	425	430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg			
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Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser			
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465	470	475	
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		Met Cys Glu Arg Pro	
		1 5	
gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt			163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val			
	10	15	20
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Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile			
	25	30	35
tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg			259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val			
	40	45	50
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct			307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala			
	55	60	65
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag			355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu			
	70	75	80
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa			403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln			
	90	95	100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
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185 190 195	
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Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
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Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
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ggg ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	
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Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
280 285 290	
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag	
1027	
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln	
295 300 305	
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc	
1075	
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly	
310 315 320 325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt	
1123	

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
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 1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

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 1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
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ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507

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 1528

Ala Ala Gly Glu Ser Val Glu  
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<210> 1124

<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

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 20 25 30



Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
                   35                                  40                                  45  
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
                   50                                  55                                  60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
                   65                                  70                                  75                                  80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
                                   85                                  90                                  95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
                                  100                                 105                                 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
                                  115                                 120                                 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
                                  130                                 135                                 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
                                  145                                 150                                 155                                 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
                                  165                                 170                                 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
                                  180                                 185                                 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
                                  195                                 200                                 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
                                  210                                 215                                 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
                                  225                                 230                                 235                                 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
                                  245                                 250                                 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
                                  260                                 265                                 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
                                  275                                 280                                 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
                                  290                                 295                                 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
                                  305                                 310                                 315                                 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
                                  325                                 330                                 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
                                  340                                 345                                 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

355					360					365					
Glu	Ser	Leu	Arg	Arg	Leu	Ala	Val	His	Val	Asp	Val	Val	Thr	Pro	Asn
370					375					380					
Ile	Pro	Glu	Leu	Ala	Val	Leu	Cys	Asp	Ser	Ala	Pro	Ala	Ile	Thr	Met
385					390					395					400
Asp	Glu	Ala	Ile	Ala	Gln	Ala	Gln	Gly	Phe	Ala	Arg	Thr	His	Asp	Thr
405					410					415					
Ile	Val	Ile	Val	Lys	Gly	Gly	His	Leu	Thr	Gly	Ala	Leu	Ala	Asp	Asn
420					425					430					
Ala	Val	Val	Arg	Pro	Asp	Gly	Ser	Val	Phe	Gln	Val	Glu	Asn	Leu	Arg
435					440					445					
Val	Asn	Thr	Thr	Asn	Ser	His	Gly	Thr	Gly	Cys	Ser	Leu	Ser	Ala	Ser
450					455					460					
Leu	Ala	Thr	Lys	Ile	Ala	Ala	Gly	Glu	Ser	Val	Glu				
465					470					475					

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<210> 1125
<211> 795
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(772)  
<223> RXN01617
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<400> 1125																		
tcagaagcta	ccggcgggcgc	cggcattccag	gttgatttga	agaccttcca	gcatttaaga												60	
tgtttatggc	attgggtcca	tcacatgctt	gggtggcctt	ttg	atc	cta	aag	aca									115	
				Leu	Ile	Leu	Lys	Thr										
				1									5					
act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat												163						
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn																		
					10						15						20	
cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc												211						
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile																		
					25						30						35	
ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg												259						
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu																		
				40						45						50		
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc												307						
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys																		
					55						60						65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc												355						
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg																		
70						75						80						85

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403  
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu  
90 95 100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451  
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu  
105 110 115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499  
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val  
120 125 130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547  
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu  
135 140 145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595  
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp  
150 155 160 165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643  
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala  
170 175 180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691  
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys  
185 190 195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739  
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro  
200 205 210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc 792  
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
215 220

cct 795

&lt;210&gt; 1126

&lt;211&gt; 224

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala  
1 5 10 15

Gln Val Ile Ala Asn Gln Ile Glu Ala Thr Ala Ala His Asp Leu  
20 25 30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
35 40 45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
50 55 60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
65 70 75 80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

85								90					95			
Pro	Asn	Asn	Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu	
			100					105					110			
Thr	Ile	Asp	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly	
		115					120					125				
Pro	Gln	Tyr	Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn	
	130					135					140					
Ala	Val	Asp	Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu	
145					150					155					160	
Pro	Lys	Ile	Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala	
				165					170					175		
Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala	
			180					185					190			
Val	Thr	Thr	Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val	
		195					200					205				
Ala	Ser	Asn	Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys	
	210					215					220					

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<210> 1127
<211> 638
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1) .. (615)  
<223> FRXA01617
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<400> 1127																	
gct	aat	cag	att	gag	gcc	gcc	acc	gca	gcg	cac	gat	ctt	gat	gtg	gtg	48	
Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val		
1				5					10					15			
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96	
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr		
			20					25					30				
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144	
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu		
		35					40					45					
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192	
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala		
	50					55					60						
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	240	
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn		
65					70					75				80			

```

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
                        85                        90                        95

gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
                        100                        105                        110

gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
                        115                        120                        125

gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
                        130                        135                        140

ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
145                        150                        155                        160

acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
                        165                        170                        175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
                        180                        185                        190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
                        195                        200                        205

aaacaagctc cct 638

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&lt;210&gt; 1128

&lt;211&gt; 205

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1128

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Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1                        5                        10                        15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
                20                        25                        30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35                        40                        45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50                        55                        60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65                        70                        75                        80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
                85                        90                        95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
100                        105                        110

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Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
 195 200 205

&lt;210&gt; 1129

&lt;211&gt; 792

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(769)

&lt;223&gt; RXC01600

&lt;400&gt; 1129

tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tgc aag atg 115  
 Met Val Ser Lys Met  
 1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163  
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu  
 10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211  
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro  
 25 30 35

ggg ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259  
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val  
 40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307  
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr  
 55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355  
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu  
 70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403  
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met  
 90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451  
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu  
 105 110 115  
  
 att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499  
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala  
 120 125 130  
  
 cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547  
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu  
 135 140 145  
  
 gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595  
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met  
 150 155 160 165  
  
 gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643  
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met  
 170 175 180  
  
 gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691  
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr  
 185 190 195  
  
 gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739  
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala  
 200 205 210  
  
 cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789  
 His Gly Ile Val Pro Asp Met Lys Lys Leu  
 215 220  
  
 aaa 792

&lt;210&gt; 1130

&lt;211&gt; 223

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr  
 1 5 10 15  
  
 Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp  
 20 25 30  
  
 Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu  
 35 40 45  
  
 His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala  
 50 55 60  
  
 Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu  
 65 70 75 80  
  
 Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala  
 85 90 95  
  
 Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser  
 100 105 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val  
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val  
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His  
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala  
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser  
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala  
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu  
 210 215 220

&lt;210&gt; 1131

&lt;211&gt; 726

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; RXC01622

&lt;400&gt; 1131

aaggcggtggg cggtttttgaa ggagcttcgt ttggagcgcg gtcctttgga tcgtgaagtt 60

gccatcgtag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115  
 Met Ser Asp Phe Tyr  
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163  
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly  
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211  
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg  
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259  
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val  
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307  
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu  
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355  
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro  
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403



Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val  
 90 95 100  
 gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451  
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val  
 105 110 115  
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499  
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu  
 120 125 130  
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547  
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu  
 135 140 145  
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595  
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro  
 150 155 160 165  
 tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643  
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met  
 170 175 180  
 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691  
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp  
 185 190 195  
 cct tca gat aat tagatgagtt ccgaaaattt aaa 726  
 Pro Ser Asp Asn  
 200

&lt;210&gt; 1132

&lt;211&gt; 201

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn  
 1 5 10 15  
 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser  
 20 25 30  
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala  
 35 40 45  
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala  
 50 55 60  
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu  
 65 70 75 80  
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val  
 85 90 95  
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu  
 100 105 110  
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val  
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp  
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val  
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile  
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser  
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn  
 195 200

&lt;210&gt; 1133

&lt;211&gt; 1827

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1804)

&lt;223&gt; RXC00128

&lt;400&gt; 1133

ccattttccg tttggtcttg cctaaagaac cgcattggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115  
 Val Ser Lys Ile Ser  
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163  
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val  
 10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211  
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg  
 25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259  
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro  
 40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307  
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
 55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly  
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403  
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499  
 Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr  
 120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547  
 Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu  
 135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595  
 Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu  
 150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643  
 Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe  
 170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat 691  
 Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn  
 185 190 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739  
 Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly  
 200 205 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787  
 Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp  
 215 220 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg 835  
 Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu  
 230 235 240 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg 883  
 Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val  
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931  
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala  
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979  
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp  
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg  
 1027  
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu  
 295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg  
 1075  
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val  
 310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg  
 1123  
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala  
 330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac  
 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
 1219  
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg  
 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
 1507  
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
 1555  
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
 1603  
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
 1651  
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc  
1827

Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

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Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545              550              555              560

Arg Ala Ala Pro Val Val Ala Tyr
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<210> 1135
<211> 555
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(532)
<223> RXC01709

<400> 1135
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gaaattaggt gtcgatgcag caatacggaa ctttgccaat gtg ttt gaa caa gct 115
              Val Phe Glu Gln Ala
              1              5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg 163
Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly
              10              15              20

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc 211
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser
              25              30              35

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca 259
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala
              40              45              50

cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc 307
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr
              55              60              65

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa 355
Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
70              75              80              85

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
              90              95              100

atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
              105              110              115

tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
              120              125              130

atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
              135              140

```

gat

555

&lt;210&gt; 1136

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1136

Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly  
 1 5 10 15

Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser  
 20 25 30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly  
 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg  
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys  
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser  
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser  
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu  
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser  
 130 135 140

&lt;210&gt; 1137

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(898)

&lt;223&gt; RXC02207

&lt;400&gt; 1137

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ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115  
 Met Arg Arg Arg Ser  
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163  
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala  
 10 15 20



ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg	211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met	
25 30 35	
ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc	259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly	
40 45 50	
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt	307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly	
55 60 65	
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc	355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val	
70 75 80 85	
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa	403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln	
90 95 100	
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc	451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala	
105 110 115	
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg	499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu	
120 125 130	
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat	547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp	
135 140 145	
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc	595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg	
150 155 160 165	
gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag	643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln	
170 175 180	
ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc	691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr	
185 190 195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt	739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg	
200 205 210	
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt	787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly	
215 220 225	
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att	835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile	
230 235 240 245	
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc	883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro	
250 255 260	

cac cga cga gga acc  
His Arg Arg Gly Thr  
265

898

&lt;210&gt; 1138

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1138

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu  
1 5 10 15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr  
20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala  
35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met  
50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu  
65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu  
85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe  
100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro  
115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala  
130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu  
145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala  
165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp  
180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp  
195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val  
210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu  
225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu  
245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr  
260 265

&lt;210&gt; 1139

&lt;211&gt; 891

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(868)

&lt;223&gt; RXA00347

&lt;400&gt; 1139

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aaagtgccag	gggttctgtg	ggatccgtac	actgggttccc	atg	act	ttg	act	att	115
				Met	Thr	Leu	Thr	Ile	
				1				5	

gag	gaa	atc	gcc	aag	acc	aaa	aag	ctt	ttg	ggt	gtg	tcc	gat	ttt	gat	163
Glu	Glu	Ile	Ala	Lys	Thr	Lys	Lys	Leu	Leu	Val	Val	Ser	Asp	Phe	Asp	
				10				15						20		

gga	acc	atc	gca	gga	ttt	agc	aag	gac	gct	tac	aac	gtt	cct	atc	aac	211
Gly	Thr	Ile	Ala	Gly	Phe	Ser	Lys	Asp	Ala	Tyr	Asn	Val	Pro	Ile	Asn	
			25					30					35			

cag	aaa	tcc	ctc	aag	gcg	gta	aaa	gac	ctc	tcc	caa	caa	gca	gac	act	259
Gln	Lys	Ser	Leu	Lys	Ala	Val	Lys	Asp	Leu	Ser	Gln	Gln	Ala	Asp	Thr	
		40					45					50				

gat	gtt	gtc	att	ttg	tcg	gga	cgt	cac	ctg	gag	gga	ttg	aag	acg	gtt	307
Asp	Val	Val	Ile	Leu	Ser	Gly	Arg	His	Leu	Glu	Gly	Leu	Lys	Thr	Val	
	55					60					65					

ctt	gat	ctt	ggt	cag	tac	gac	atc	acc	atg	gtg	ggt	tca	cac	ggt	tct	355
Leu	Asp	Leu	Gly	Gln	Tyr	Asp	Ile	Thr	Met	Val	Gly	Ser	His	Gly	Ser	
70				75					80					85		

gag	gat	tcc	tcc	cgc	ccg	cgt	acc	ctc	act	cct	gaa	gag	gta	gct	cgc	403
Glu	Asp	Ser	Ser	Arg	Pro	Arg	Thr	Leu	Thr	Pro	Glu	Glu	Val	Ala	Arg	
				90					95					100		

ctc	gcc	aag	att	gaa	gca	gat	ctg	gaa	aag	atc	gtc	gac	ggc	atc	gaa	451
Leu	Ala	Lys	Ile	Glu	Ala	Asp	Leu	Glu	Lys	Ile	Val	Asp	Gly	Ile	Glu	
		105					110					115				

ggc	gca	ttc	gtg	gag	atc	aag	cct	ttc	cac	cgc	gtg	ctg	cac	ttc	atc	499
Gly	Ala	Phe	Val	Glu	Ile	Lys	Pro	Phe	His	Arg	Val	Leu	His	Phe	Ile	
		120				125						130				

cgt	gtt	tcc	gac	aag	gac	aaa	gtc	caa	gga	atc	ctc	gcc	caa	gca	gca	547
Arg	Val	Ser	Asp	Lys	Asp	Lys	Val	Gln	Gly	Ile	Leu	Ala	Gln	Ala	Ala	
	135					140					145					

cac	gta	gac	tct	tcc	ggc	ctg	aag	gtt	act	aac	ggc	aag	agc	atc	atc	595
His	Val	Asp	Ser	Ser	Gly	Leu	Lys	Val	Thr	Asn	Gly	Lys	Ser	Ile	Ile	
150					155				160					165		

gaa	tac	tcc	atc	agc	tcc	acc	acc	aag	ggc	acc	tgg	ctg	aag	gaa	tac	643
Glu	Tyr	Ser	Ile	Ser	Ser	Thr	Thr	Lys	Gly	Thr	Trp	Leu	Lys	Glu	Tyr	

170	175	180	
gtt gac cgc acc gag ccc act ggt gtg att ttc ctc ggc gat gac acc			691
Val Asp Arg Thr Glu Pro Thr Gly	Val Ile Phe Leu Gly	Asp Asp Thr	
185	190	195	
acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta			739
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu			
200	205	210	
acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac			787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp			
215	220	225	
gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc			835
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg			
230	235	240	245
atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaacgcacg			888
Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile			
250	255		
aaa			891
 <210> 1140			
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<213> Corynebacterium glutamicum			
 <400> 1140			
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Val Ser Asp Phe Asp Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr			
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Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser			
35	40	45	
Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu			
50	55	60	
Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val			
65	70	75	80
Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro			
85	90	95	
Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile			
100	105	110	
Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg			
115	120	125	
Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile			
130	135	140	
Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn			
145	150	155	160

Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr  
 165 170 175  
 Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe  
 180 185 190  
 Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn  
 195 200 205  
 Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala  
 210 215 220  
 Lys Thr Arg Val Asp Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys  
 225 230 235 240  
 Leu Ala Tyr His Arg Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile  
 245 250 255

<210> 1141  
 <211> 2556  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(2533)  
 <223> RXN01239

<400> 1141  
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 gtaccgcacg attttgcta acttttaagg gtgtttcatc atg gca cgt cca att 115  
 Met Ala Arg Pro Ile  
 1 5  
 tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163  
 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala  
 10 15 20  
 ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg 211  
 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu  
 25 30 35  
 aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259  
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala  
 40 45 50  
 atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307  
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile  
 55 60 65  
 aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355  
 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala  
 70 75 80 85  
 aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403  
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His

	90	95	100	
tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta				451
Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu				
	105	110	115	
aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg				499
Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp				
	120	125	130	
cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt				547
His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly				
	135	140	145	
gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag				595
Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu				
	150	155	160	165
aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc				643
Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr				
	170	175	180	
gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg				691
Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu				
	185	190	195	
cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg				739
Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val				
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aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat				787
Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His				
	215	220	225	
act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc				835
Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly				
	230	235	240	245
gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg				883
Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu				
	250	255	260	
cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa				931
His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu				
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aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat				979
Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp				
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1027				
Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile				
	295	300	305	
tcc cga gaa tct gag gac aaa ttc tcc atg ctg gcg ctg acc cac agt				
1075				
Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser				
	310	315	320	325

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 Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu  
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 Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu  
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gcc cgc gcc atg cgc cgc gat aac ttc tcc acc gca ggc acc aac gtc  
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 Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val  
                   360                                  365                                  370

acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg  
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 Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met  
                   375                                  380                                  385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc  
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 Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr  
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gtc atc gcg gag atg tcc aaa cgc ttc ccc tcc cgg cgt gac gca ctc  
 1363  
 Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu  
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 Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg  
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 Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr  
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acc ttc tac cgc gca tct agg ctc gtt gca ttg caa gaa gtc ggt ggc  
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 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly  
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 1555  
 Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln  
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 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg  
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 2131  
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 680 685 690

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 2227  
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala  
 695 700 705



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2275

Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly  
710 715 720 725

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2323

Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp  
730 735 740

cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc  
2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile  
745 750 755

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2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly  
760 765 770

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Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val  
775 780 785

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2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu  
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<213> *Corynebacterium glutamicum*

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Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
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Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
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Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
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Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Phe	Asp	Ile	Asp	Trp	His	Glu	Asp	Asn	Gly	Ser	Gly	Gly	Lys	Leu	Gly
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Met	Pro	Ile	Leu	Gly	Ala	Glu	Gly	Asp	Glu	Asp	Lys	Leu	Glu	Phe	Ala
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Glu	Leu	Asp	Gly	Glu	Lys	Val	Leu	Lys	Tyr	Phe	Asp	His	Leu	Phe	Pro
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Ile	Ala	Pro	Gly	Thr	Glu	Glu	Gly	Thr	Pro	Gln	Glu	Val	Tyr	Lys	Arg
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Gln	His	Tyr	Arg	Leu	Gln	Phe	Trp	Arg	Asp	Gly	Val	Ile	Asn	Phe	Arg
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Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Asp	His	Pro	Asp	Gly	Leu	Ser	Asp
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Pro	Phe	Gly	Tyr	Leu	His	Arg	Leu	Arg	Asp	Leu	Ile	Gly	Pro	Asp	Arg
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Trp	Leu	Ile	Ile	Glu	Lys	Ile	Leu	Ser	Val	Asp	Glu	Pro	Leu	Asp	Pro
		275					280					285			
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	290					295					300				
Asp	Gly	Val	Phe	Ile	Ser	Arg	Glu	Ser	Glu	Asp	Lys	Phe	Ser	Met	Leu
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Ala	Leu	Thr	His	Ser	Gly	Ser	Thr	Trp	Asp	Glu	Arg	Ala	Leu	Lys	Ser
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Thr	Glu	Glu	Ser	Leu	Lys	Arg	Val	Val	Ala	Gln	Gln	Glu	Leu	Ala	Ala
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Arg	Thr	Thr	Ala	Thr	Val	Ile	Ala	Glu	Met	Ser	Lys	Arg	Phe	Pro	Ser
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Arg	Arg	Asp	Ala	Leu	Asp	Leu	Ile	Ala	Ala	Ala	Leu	Leu	Gly	Asn	Gly
			420					425					430		

Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
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Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
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Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
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Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
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Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
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Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
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Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
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Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
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Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
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Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
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Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
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Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile  
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Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
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Glu Arg Leu Gln Thr Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp  
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Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser  
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Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
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Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
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Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
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Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
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Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
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aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259  
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 120 125 130

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His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly	
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Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu	
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Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr	
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Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val	
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Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His	
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Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly	
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Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu	
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His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu	
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Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp	
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1555
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gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg
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cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg
1651
His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
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1747
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cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc  
2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile  
745 750 755

ttg gaa gac cgt ggc gga tgg tat gac acc acc gtc acg ctt cct ggt  
2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly  
760 765 770

gga caa tgg gaa gac agg ctc acc ggg caa cgc ttc agt ggt gtt gtc  
2467

Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val  
775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta  
2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu  
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2556

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810

<210> 1144

<211> 811

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1144

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20 25 30

Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser  
35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp  
100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr  
115 120 125

Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly  
130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala  
145 150 155 160



Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro  
 165 170 175  
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg  
 180 185 190  
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg  
 195 200 205  
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro  
 210 215 220  
 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu  
 225 230 235 240  
 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp  
 245 250 255  
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg  
 260 265 270  
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro  
 275 280 285  
 Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu  
 290 295 300  
 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu  
 305 310 315 320  
 Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser  
 325 330 335  
 Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala  
 340 345 350  
 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr  
 355 360 365  
 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu  
 370 375 380  
 Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser  
 385 390 395 400  
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser  
 405 410 415  
 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly  
 420 425 430  
 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
 435 440 445  
 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
 450 455 460  
 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
 465 470 475 480

Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
 485 490 495  
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
 500 505 510  
 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
 515 520 525  
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser  
 530 535 540  
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
 545 550 555 560  
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
 565 570 575  
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
 580 585 590  
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
 595 600 605  
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
 610 615 620  
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile  
 625 630 635 640  
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp  
 645 650 655  
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
 660 665 670  
 Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp  
 675 680 685  
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser  
 690 695 700  
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
 705 710 715 720  
 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
 725 730 735  
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
 740 745 750  
 Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
 755 760 765  
 Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
 770 775 780  
 Phe Ser Gly Val Val Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val  
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 Ser Leu Leu Val Leu Val Pro Asp Ser Glu Phe

805

810

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<211> 1953
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1930)
<223> RXA02645
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<400> 1145

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Met Leu Lys Asp Leu  
1 5

acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca 163  
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser  
10 15 20

cat ctt agc tgc cca acc ggc agc att ttc act agc ctg gtg gcc atg 211  
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met  
25 30 35

ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta 259  
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val  
40 45 50

cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc 307  
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly  
55 60 65

agc tgg tgg cgc gcc gag atc gcg ccc aag gcc ggc gat cgt tac ggt 355  
 Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly  
 70 75 80 85

ttt tcg ctt ttc gac ggc tcc tcc tgg tca aaa acc ctc ccc gat ccc 403  
Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro  
90 95 100

cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc 451  
 Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser  
 105 110 115

gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc 499  
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu  
120 125 130

cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat 547  
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp  
135 140 145

gga acg ttt gag gga gtc gtc gac aag ctt cct tat ctg cgc gac ctc 595  
Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu  
150 155 160 165

ggc gtg acc gcc atc gaa ctt tta ccc gtg cag ccc ttt ggc ggc aac 643

Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln Pro Phe Gly Gly Asn	
170 175 180	
cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc	691
Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly	
185 190 195	
tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag	739
Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln	
200 205 210	
gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc	787
Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro	
215 220 225	
gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc	835
Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser	
230 235 240 245	
acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa	883
Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu	
250 255 260	
gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt	931
Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe	
265 270 275	
cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc	979
His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg	
280 285 290	
ggc gcc tat tcc cta ctt gcg cag ctg acc atg gtg gcc gag gat gtc	
1027	
Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val	
295 300 305	
tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc	
1075	
Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu	
310 315 320 325	
aat gac ccc aag ttc gtt acc tcc cgc gag gcc ggc ggt ttt ggc ctg	
1123	
Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu	
330 335 340	
gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt	
1171	
Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val	
345 350 355	
tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca	
1219	
Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr	
360 365 370	
tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc	
1267	
Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser	
375 380 385	

gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca  
1891

Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr  
585 590 595

acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg  
1940

Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr Arg Asn  
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1953

<210> 1146

<211> 610

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1146

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Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro  
35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met  
50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala  
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys  
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly  
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp  
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly  
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro  
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln  
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His  
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile  
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr  
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc  
 1315  
 Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr  
 390 395 400 405

cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc  
 1363  
 Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly  
 410 415 420

aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag  
 1411  
 Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln  
 425 430 435

cag gtg ttg aag gca gcc att atc tac agc tcg ccg tat acc ccg atg  
 1459  
 Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met  
 440 445 450

ttg ttt atg ggt gaa gaa ttc gga gcc acc acc cca ttc gcc ttc ttt  
 1507  
 Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr Pro Phe Ala Phe Phe  
 455 460 465

tgc tcc cac acc gac ccc gag ctc aac cgg cta acc tcc gag ggc cgc  
 1555  
 Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg  
 470 475 480 485

aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc  
 1603  
 Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser  
 490 495 500

ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc  
 1651  
 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe  
 505 510 515

act gcg gag cag cgc cgc atc aac gac gct tac aag cag ctg ttg cac  
 1699  
 Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His  
 520 525 530

ctg cgg cac acc ttg ggc ttc tcc caa cca aac ttg ctc aca ctc gag  
 1747  
 Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn Leu Leu Thr Leu Glu  
 535 540 545

gtt gag cac ggc gag aac tgg cta tcg atg gcc aat ggt cgc ggc cga  
 1795  
 Val Glu His Gly Glu Asn Trp Leu Ser Met Ala Asn Gly Arg Gly Arg  
 550 555 560 565

att ctg gcg aat ttc tcc gac gac acc atc acc gtc ccg ctt ggc ggc  
 1843  
 Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly  
 570 575 580

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr  
 225 230 235 240  
 Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly  
 245 250 255  
 His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln  
 260 265 270  
 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His  
 275 280 285  
 Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met  
 290 295 300  
 Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile  
 305 310 315 320  
 Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala  
 325 330 335  
 Gly Gly Phe Gly Leu Asp Ala Gln Trp Val Asp Asp Ile His His Ala  
 340 345 350  
 Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe  
 355 360 365  
 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His  
 370 375 380  
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val  
 385 390 395 400  
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr  
 405 410 415  
 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr  
 420 425 430  
 Leu Thr Pro Glu Gln Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser  
 435 440 445  
 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr  
 450 455 460  
 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu  
 465 470 475 480  
 Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala  
 485 490 495  
 Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys  
 500 505 510  
 Leu Asp Trp Glu Phe Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr  
 515 520 525  
 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn  
 530 535 540

Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala  
 545 550 555 560  
 Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr  
 565 570 575  
 Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val  
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 595 600 605  
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 <211> 832  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(832)  
 <223> RXN02355

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 Met Ser Ser Ile Ser  
 1 5  
 cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163  
 Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile  
 10 15 20  
 gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211  
 Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser  
 25 30 35  
 acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259  
 Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met  
 40 45 50  
 ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307  
 Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn  
 55 60 65  
 gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355  
 Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu  
 70 75 80 85  
 gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403  
 Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn  
 90 95 100  
 tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gac ttc 451  
 Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe  
 105 110 115



gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499  
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp  
           120                          125                          130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547  
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly  
           135                          140                          145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595  
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg  
           150                          155                          160                          165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643  
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val  
                           170                          175                          180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691  
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr  
                           185                          190                          195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739  
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile  
                           200                          205                          210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787  
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg  
           215                          220                          225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832  
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly  
           230                          235                          240

&lt;210&gt; 1148

&lt;211&gt; 244

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1148

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Leu Leu Ala Ala Ile Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser  
           20                          25                          30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro  
           35                          40                          45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile  
           50                          55                          60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn  
           65                          70                          75                          80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser  
                           85                          90                          95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile  
           100                          105                          110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115					120					125					
Asp	Leu	Glu	Val	Asp	Thr	Ser	Gly	Leu	Leu	Gln	Ser	Thr	Val	Asp	Ser
130						135					140				
Ala	Thr	Tyr	Asn	Gly	Thr	Leu	Tyr	Ala	Leu	Pro	Gln	Asn	Thr	Asn	Gly
145					150					155					160
Gln	Leu	Leu	Phe	Arg	Asn	Thr	Glu	Ile	Ile	Pro	Glu	Ala	Pro	Ala	Asn
				165					170					175	
Trp	Ala	Asp	Leu	Val	Glu	Ser	Cys	Thr	Leu	Ala	Glu	Glu	Ala	Gly	Val
			180					185					190		
Asp	Cys	Leu	Thr	Thr	Gln	Leu	Lys	Gln	Tyr	Glu	Gly	Leu	Ser	Val	Asn
	195					200						205			
Thr	Ile	Gly	Phe	Ile	Glu	Gly	Trp	Gly	Gly	Ser	Val	Leu	Asp	Asp	Asp
	210					215					220				
Gly	Lys	Arg	His	Arg	Arg	Gln	His	Asp	Gly	Lys	Ala	Gly	Leu	Gln	Ala
225					230					235					240
Leu Val Asp Gly															

&lt;210&gt; 1149

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(586)

&lt;223&gt; RXN02909

&lt;400&gt; 1149

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				Met	Asn	Arg	Ala	Arg	
				1				5	

atc	gcg	acc	ata	ggc	gtt	ctt	ccg	ctt	gct	tta	ctg	ctg	gcg	tcc	tgt	163
Ile	Ala	Thr	Ile	Gly	Val	Leu	Pro	Leu	Ala	Leu	Leu	Leu	Ala	Ser	Cys	
				10					15					20		

ggt	tca	gac	acc	gtg	gaa	atg	aca	gat	tcc	acc	tgg	ttg	gtg	acc	aat	211
Gly	Ser	Asp	Thr	Val	Glu	Met	Thr	Asp	Ser	Thr	Trp	Leu	Val	Thr	Asn	
			25					30					35			

att	tac	acc	gat	cca	gat	gag	tcg	aat	tcg	atc	agt	aat	ctt	gtc	att	259
Ile	Tyr	Thr	Asp	Pro	Asp	Glu	Ser	Asn	Ser	Ile	Ser	Asn	Leu	Val	Ile	
		40				45						50				

tcc	cag	ccc	agc	tta	gat	ttt	ggc	aat	tct	tcc	ctg	tct	ggt	ttc	act	307
Ser	Gln	Pro	Ser	Leu	Asp	Phe	Gly	Asn	Ser	Ser	Leu	Ser	Gly	Phe	Thr	
		55				60					65					

ggc	tgt	gtg	cct	ttt	acg	ggg	cgt	gcg	gaa	ttc	ttc	caa	aat	ggt	gag	355
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Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu  
 70 75 80 85  
 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403  
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp  
 90 95 100  
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451  
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His  
 105 110 115  
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499  
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr  
 120 125 130  
 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547  
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg  
 135 140 145  
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taagggtgcca 596  
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser  
 150 155 160  
 gggctttaaa gtg 609

&lt;210&gt; 1150

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1150

Met Asn Arg Ala Arg Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu  
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 Leu Leu Ala Ser Cys Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr  
 20 25 30  
 Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile  
 35 40 45  
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser  
 50 55 60  
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe  
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 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr  
 85 90 95  
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 100 105 110  
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe  
 115 120 125  
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val  
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Thr Ser

&lt;210&gt; 1151

&lt;211&gt; 1590

&lt;212&gt; DNA

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&lt;222&gt; (101)..(1567)

&lt;223&gt; RXS00349

&lt;400&gt; 1151

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gtgattggac	tcttttttct	tgcaaaatgt	tttccagcgg	atg	ttg	agt	ttt	gcg	115
				Met	Leu	Ser	Phe	Ala	
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acc	ctt	cgt	ggc	cgc	att	tca	aca	ggt	gac	gct	gca	aaa	gcc	gca	cct	163
Thr	Leu	Arg	Gly	Arg	Ile	Ser	Thr	Val	Asp	Ala	Ala	Lys	Ala	Ala	Pro	
			10					15					20			

ccg	cca	tcg	cca	cta	gcc	ccg	att	gat	ctc	act	gac	cat	agt	caa	gtg	211
Pro	Pro	Ser	Pro	Leu	Ala	Pro	Ile	Asp	Leu	Thr	Asp	His	Ser	Gln	Val	
			25				30					35				

gcc	ggt	gtg	atg	aat	ttg	gct	gcg	aga	att	ggc	gat	att	ttg	ctt	tct	259
Ala	Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly	Asp	Ile	Leu	Leu	Ser	
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tca	ggt	acg	tca	aat	agt	gac	acc	aag	gta	caa	ggt	cga	gca	gtg	acc	307
Ser	Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln	Val	Arg	Ala	Val	Thr	
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tct	gcg	tac	ggt	ttg	tac	tac	acg	cac	gtg	gat	atc	acg	ttg	aat	acg	355
Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr	
70				75					80				85			

atc	acc	atc	ttc	acc	aac	atc	ggt	gtg	gag	agg	aag	atg	ccg	gtc	aac	403
Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn	
			90				95						100			

gtg	ttt	cat	ggt	gta	ggc	aag	ttg	gac	acc	aac	ttc	tcc	aaa	ctg	tct	451
Val	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser	
			105				110						115			

gag	ggt	gac	cgt	ttg	atc	cgt	tcc	att	cag	gct	ggt	gcg	acc	ccg	cct	499
Glu	Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	Gly	Ala	Thr	Pro	Pro	
		120				125					130					

gag	ggt	gcc	gag	aaa	atc	ctg	gac	gag	ttg	gag	caa	tcc	cct	gcg	tct	547
Glu	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser	
		135				140					145					

tat	ggt	ttc	cct	ggt	gcg	ttg	ctt	ggc	tgg	gca	atg	atg	ggt	ggt	gct	595
Tyr	Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	Met	Met	Gly	Gly	Ala	
150				155					160						165	

gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt 643  
 Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe  
 170 175 180

att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag 691  
 Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys  
 185 190 195

ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg 739  
 Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr  
 200 205 210

ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag 787  
 Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu  
 215 220 225

atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca 835  
 Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala  
 230 235 240 245

ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg 883  
 Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro  
 250 255 260

gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc 931  
 Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly  
 265 270 275

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 Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly  
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ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt  
 1219  
 Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly  
 360 365 370

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 1267  
 Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile

375                      380                      385  
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg  
 1315  
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met  
 390                      395                      400                      405  
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg  
 1363  
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala  
 410                      415                      420  
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt  
 1411  
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly  
 425                      430                      435  
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac  
 1459  
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr  
 440                      445                      450  
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag  
 1507  
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu  
 455                      460                      465  
 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc  
 1555  
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe  
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 Gly Asn Lys Arg

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 <213> *Corynebacterium glutamicum*

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 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly  
 35                      40                      45  
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
 50                      55                      60  
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
 65                      70                      75                      80  
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
 85                      90                      95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
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 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
 115 120 125  
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
 130 135 140  
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala  
 145 150 155 160  
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val  
 165 170 175  
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
 180 185 190  
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
 195 200 205  
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
 210 215 220  
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
 225 230 235 240  
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
 245 250 255  
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu  
 260 265 270  
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu  
 275 280 285  
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
 290 295 300  
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 325 330 335  
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe  
 340 345 350  
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
 355 360 365  
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
 370 375 380  
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
 405 410 415

Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
 420 425 430  
 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
 435 440 445  
 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
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 aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96  
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30  
 aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144  
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45  
 atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60  
 cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240  
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80  
 cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95  
 cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110  
 gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125  
 gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437  
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ttc 440

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 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60  
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
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 Met Ser Ile Gly Gln  
 1 5  
 cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163  
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp  
 10 15 20  
 aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala	
25 30 35	
gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat	259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp	
40 45 50	
ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc	307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe	
55 60 65	
gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca	355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro	
70 75 80 85	
ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa	403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys	
90 95 100	
gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat	451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp	
105 110 115	
gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc	499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile	
120 125 130	
ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc	547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val	
135 140 145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg	595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu	
150 155 160 165	
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa	643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu	
170 175 180	
gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg	691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg	
185 190 195	
gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat	739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn	
200 205 210	
gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc	787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala	
215 220 225	
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Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile	
230 235 240 245	
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac	883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr	
250 255 260	
atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga	931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg	

265 270 275  
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 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser  
 280 285 290  
 atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac  
 1027  
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 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln  
 310 315 320 325  
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 330 335 340  
 tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg  
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 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala  
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 Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu  
 35 40 45  
 Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu  
 50 55 60  
 Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile  
 65 70 75 80  
 Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile  
 85 90 95  
 Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser  
 100 105 110  
 Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro  
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala  
 130 135 140  
 Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly  
 145 150 155 160  
 Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala  
 165 170 175  
 Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser  
 180 185 190  
 Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu  
 195 200 205  
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 210 215 220  
 Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala  
 225 230 235 240  
 His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys  
 245 250 255  
 Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg  
 260 265 270  
 Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala  
 275 280 285  
 Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His  
 290 295 300  
 Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly  
 305 310 315 320  
 Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala  
 325 330 335  
 Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys  
 340 345 350  
 Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp  
 355 360

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- (72) Inventors: POMPEJUS, Markus; Wenjenstr. 21, D-67251 Freinsheim (DE). KRÖGER, Burkhard; Im Waldhof 1, D-67117 Limburgerhof (DE). SCHRÖDER, Hartwig; Goethestr. 5, D-69226 Nussloch (DE). ZELDER, Oskar; Rossmarktstr. 27, D-67346 Speyer (DE). HABERHAUER, Gregor; Moselstr. 42, D-67117 Limburgerhof (DE).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,

[Continued on next page]

(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.



IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(88) Date of publication of the international search report:  
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**Published:**

— *With international search report.*

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*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00923

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/61 C12N1/21 C12N9/90 C07K14/34  
 C12P13/08 C12Q1/68  
 //(C12N15/61,C12R1:15)

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12P C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, EMBL, BIOSIS

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>KEILHAUER C ET AL: "ISOLEUCINE SYNTHESIS IN CORYNEBACTERIUM GLUTAMICUM: MOLECULAR ANALYSIS OF THE ILVB-ILVN-ILVC OPERON" JOURNAL OF BACTERIOLOGY,US,WASHINGTON, DC, vol. 175, no. 17, 1 September 1993 (1993-09-01), pages 5595-5603, XP000611312 ISSN: 0021-9193 the whole document</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	<p>1-3, 8-19, 22-34</p>



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

## \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

31 October 2000

Date of mailing of the international search report

24. 01. 01

Name and mailing address of the ISA

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Galli, I

## INTERNATIONAL SEARCH REPORT

International Application No

PC., IB 00/00923

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL SEQUENCES [Online]  Accession No. 033231,  15 December 1998 (1998-12-15)  COLE S.T.: "Diaminopimelate epimerase  (DAPf) of Mycobacterium tuberculosis."  XP002151647  52% identity at amino acid level with Seq.  ID 2.  -&amp; COLE S.T. ET AL.: "Deciphering the  biology of Mycobacterium tuberculosis from  the complete genome sequence."  NATURE,  vol. 393, 1998, pages 537-544, XP002151645</p> <p>---</p>	6-17,37, 38
A	<p>BATHE B. ET AL.: "A physical and genetic  map of the Corynebacterium glutamicum  ATCC13032 chromosome."  MOL. GEN. GENET.,  vol. 252, 1996, pages 255-265, XP002151646  the whole document, in particular table 3.</p> <p>---</p>	1-38
A	<p>EP 0 435 132 A (KERNFORSCHUNGSANLAGE  JUELICH) 3 July 1991 (1991-07-03)  the whole document</p> <p>---</p>	1-38
A	<p>EIKMANN B J ET AL: "MOLECULAR ASPECTS OF  LYSINE, THREONINE, AND ISOLEUCINE  BIOSYNTHESIS IN CORYNEBACTERIUM  GLUTAMICUM"  ANTONIE VAN LEEUWENHOEK,DORDRECHT,NL,  vol. 64, no. 2, 1993, pages 145-163,  XP000918559  figure 1</p> <p>-----</p>	1-38



# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 00/00923

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-38 Partially.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-38, partly

An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein or a portion thereof, said nucleic acid being characterized by sequence ID 1. An isolated nucleic acid comprising a nucleotide sequence at least 50% homologous to seq. 1. Corresponding polypeptides (Seq. ID 2). Corresponding vectors, recombinant host cells, production methods. Use in diagnosis of *C. diphtheriae*.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC., iB 00/00923

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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